

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
1 April 2004 (01.04.2004)

PCT

(10) International Publication Number
WO 2004/026888 A2

(51) International Patent Classification⁷:

C07H

(72) Inventors; and

(21) International Application Number:

PCT/US2003/029577

(75) Inventors/Applicants (for US only):

LIPFORD, Grayson, B. [US/US]; 38 Bates Road, Watertown, MA 02472 (US). **MOOKHERJEE, Neeloffer** [IN/CA]; Apt 408, 2233 Allison Road., Vancouver, BC V6T 1T7 (CA). **BABIUK, Lorne** [CA/CA]; 245 East Place, Saskatoon, Saskatchewan S7J 2Y1 (CA). **BROWNLIE, Robert** [CA/CA]; 123 O'Brien Crescent, Saskatoon, Saskatchewan S7K 5K3 (CA). **GRIEBEL, Philip** [CA/CA]; Box 36, RR5, Saskatoon, Saskatchewan S7K 3J8 (CA). **MUTWIRI, George** [CA/CA]; 569 Nordstrum Road, Saskatoon, Saskatchewan S7K 7X6 (CA). **HECKER, Rolf** [DE/DE]; Benrodestr. 60, 40597 Düsseldorf (DE).

(22) International Filing Date:

19 September 2003 (19.09.2003)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

60/412,479 19 September 2002 (19.09.2002) US

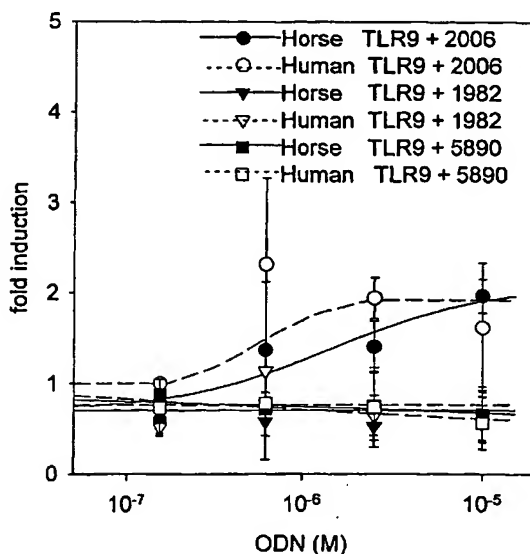
(74) Agent: **STEELE, Alan, W.**; Wolf, Greenfield & Sacks, P.C., 600 Atlantic Avenue, Boston, MA 02210 (US).

(71) Applicants (for all designated States except US): **COLEY PHARMACEUTICAL GMBH** [DE/DE]; Elisabeth-Selbert-Strasse 9, 40764 Langenfeld (DE). **UNIVERSITY OF SASKATCHEWAN** [CA/CA]; Kirk Hall, 117 Science Place, Saskatoon, Saskatchewan S7N 5C8 (CA). **QIAGEN GMBH** [DE/DE]; Max-Volmer-Strasse 4, 40724 Hilden (DE).

(81) Designated States (national): AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX,

[Continued on next page]

(54) Title: TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES



(57) Abstract: Novel amino acid and nucleotide sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) Toll-like receptor 9 (TLR9) are provided. Also provided are amino acid and nucleotide sequences for dog (canine), cat (feline), mouse (murine), and human TLR9. Comparison of these sequences, especially in combination with functional assessment for species-specific CpG motif preferences, permits identification of specific regions and amino acid residues of interest in TLR9 ligand interaction. Novel chimeric TLR9 receptor molecules, cells expressing these molecules, and methods for their use in screening assays for TLR9 ligands are also provided.



MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

- (84) **Designated States (regional):** ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO,

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

Background of the Invention

Synthetic oligodeoxynucleotides (ODN) and DNA containing immunostimulatory
5 CpG motifs (CpG DNA) function as potent adjuvants and activators of the innate immune
system. Heeg K et al. (2000) *Int Arch Allergy Immunol* 121:87-97; Krieg AM (2001)
Vaccine 19:618-22. A wide variety of CpG-containing sequences have been screened for
biological activity and it is reported that optimal CpG DNA sequences can vary among
species. Rankin R et al. (2001) *Antisense Nucleic Acid Drug Dev* 11:333-40.
10 Toll-like receptor 9 (TLR9) has recently been identified as a receptor for CpG ODN.
Hemmi H et al. (2000) *Nature* 408:740-5. The molecular mechanism by which TLR9
recognizes CpG DNA is not understood.

Summary of the Invention

15 Toll-like receptor 9 (TLR9) is known to be involved in innate immunity and to signal
in response to CpG DNA. To date, the amino acid sequences only of human and murine
TLR9 have been reported, and, interestingly, these two species are known to prefer different
CpG motifs. The structural basis for this species-specific CpG motif preference has not yet
been fully elucidated. The instant invention provides, in part, novel amino acid and
20 nucleotide sequences of rat, pig, cow, and horse TLR9. These novel TLR9 sequences are
useful for elucidating certain key structural features of TLR9. Specifically, comparison of
sequences of murine, human, and these novel TLR9 sequences permits identification of areas
of highly conserved sequence, areas of group conservation, and areas of hypervariability. In
addition, such comparisons permit an assessment of evolutionary relatedness among TLR9
25 molecules of the various species, as well as an assessment of inter-species homologies.
Importantly, such comparisons permit a rational basis for identifying amino acids in TLR9
that may be involved in the CpG binding site, as well as amino acids involved in conferring
species specificity for particular CpG motifs. Such information may be used to design and
construct novel TLR9 molecules which incorporate specific point or regional mutations and
30 which possess desired ligand binding characteristics. Such information may also be useful in
designing and identifying novel ligands for TLR9 of a given species.

- 2 -

In one aspect, the invention provides isolated polypeptides having amino acid sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) TLR9 polypeptides. These amino acid sequences correspond to SEQ ID NOs 1, 5, 9, 13, and 17, respectively. Each of these sequences is believed to include at least a majority of an extracellular domain, as well as a transmembrane region and at least part of a TLR/IL-1 receptor (TIR) domain. To the extent any such sequence may lack an amino-terminal and/or carboxy-terminal sequence, such sequence is ascertainable, without undue experimentation, using conventional molecular biology techniques and the sequence information provided herein.

10 In another aspect the invention provides isolated polypeptides having amino acid sequences for essentially the whole extracellular domain, optionally including a signal peptide, of each of rat, porcine, bovine, equine, and ovine TLR9. These amino acid sequences correspond to SEQ ID NOs 2, 6, 10, 14, and 18, respectively. Such extracellular domains are believed to include sequence specifically involved in binding to TLR9 ligand, such as CpG DNA. In addition, such extracellular domains are believed to include sequence
15 that confers species specificity for particular CpG motifs.

Isolated nucleic acid molecules encoding the polypeptides just described above are also provided according to further aspects of the invention. Such nucleic acid molecules include, but are not limited to, nucleic acid molecules having sequences provided by SEQ ID
20 NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively. Isolated nucleic acid molecules encoding the TLR9 polypeptides of SEQ ID NOs 1, 5, 9, 13, 17; and 2, 6, 10, 14, and 18 also include nucleic acid molecules that differ in sequence from SEQ ID NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively, due to degeneracy of the genetic code. Such nucleic acid molecules will hybridize, under stringent conditions, with suitably selected nucleic acid
25 molecules having sequences selected from SEQ ID NOs 3, 4, 7, 8, 11, 12, 15, 16, 19, and 20.

In another aspect the invention provides a vector which includes an isolated nucleic acid molecule of the invention. In one embodiment the vector is an expression vector and the isolated nucleic acid molecule of the invention is operably linked to a regulatory sequence in the vector. When present within a cell, an expression vector according to this aspect of the
30 invention causes the cell to express a polypeptide of the invention.

The invention according to another aspect provides a cell in which a vector of the invention is present. In one embodiment the cell containing the vector expresses a

- 3 -

polypeptide of the invention. In certain embodiments the cell also contains a reporter construct that transduces a TLR9-mediated signal in response to contact of the polypeptide of the invention or a TLR9 with a suitable TLR9 ligand. The cell containing the vector, and optionally containing the reporter construct, can be used in screening methods also provided
5 by the invention.

In yet another aspect the invention provides an antibody or antibody fragment that binds specifically to an isolated polypeptide of the invention. In certain embodiments the antibody or antibody fragment binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide. More specifically, the antibody or antibody fragment binds uniquely to
10 one of the isolated polypeptides of the invention. In one embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide also binds to either mouse or human TLR9. In another embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide does not also bind to either mouse or human TLR9. In some embodiments
15 the antibody or antibody fragment binds selectively to a chimeric TLR9 polypeptide of the invention. In certain embodiments the antibody or antibody fragment of the invention is a monoclonal antibody or fragment of a monoclonal antibody.

In one aspect the invention provides a method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the first species. The method involves aligning protein sequences of TLR9 of a first species,
20 TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species; generating an initial set of candidate amino acids in the TLR9 of the first species by excluding each amino acid in the TLR9 of the first species which (a) is
25 identical with the TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with the TLR9 of the third species or (b)
30 differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

- 4 -

In another aspect the invention provides a method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9. The method according to this aspect of the invention involves aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a CpG DNA optimized for murine TLR9; generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids. In one embodiment the method according to this aspect of the invention is performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred CpG DNA).

In another aspect the invention also provides an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (extracellular domain (ECD) of murine TLR9) except for substitution of at least one key amino acid identified according to the method above. The polypeptide according to this aspect of the invention is a chimeric TLR9 polypeptide. Preferably the polypeptide according to this aspect of the invention binds to CpG DNA optimized for human TLR9 better than does the isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (ECD of murine TLR9). In one embodiment the polypeptide includes only one substituted amino acid. The isolated polypeptide according to this aspect of the invention may further include sequence involved in TLR/IL-1R signal transduction, e.g., intracellular domain of TLR9 as provided in SEQ ID NOs 29 and 33. For example, in one embodiment a polypeptide according to this aspect of the invention is an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:29 (full length murine TLR9) except for substitution of at least one key amino acid identified according to the method above.

- 5 -

In another aspect the invention provides an isolated nucleic acid molecule including a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described. In one embodiment the isolated nucleic acid molecule has a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described.

5 In yet another aspect, the invention provides a screening method to identify a TLR9 ligand. The method involves contacting a polypeptide (including a chimeric TLR9 polypeptide) of the invention with a candidate TLR9 ligand; measuring a signal in response to the contacting; and identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling. In one embodiment
10 the candidate TLR9 ligand is an immunostimulatory nucleic acid. In one embodiment the candidate TLR9 ligand is a CpG DNA.

The invention also provides, in yet a further aspect, a screening method to identify species-specific CpG-motif preference of an isolated polypeptide of the invention. The method according to this aspect of the invention involves contacting an isolated polypeptide
15 of the invention with a CpG DNA including a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG; measuring a signal in response to the contacting; and identifying a species-specific CpG-motif preference when the signal in
20 response to the contacting is consistent with TLR9 signaling. In one embodiment the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

	TCCATGACGTTTTTGATGTT	(SEQ ID NO:39),
	TCCATAACGTTTTTGATGTT	(SEQ ID NO:40),
	TCCATCACGTTTTTGATGTT	(SEQ ID NO:41),
25	TCCATTACGTTTTTGATGTT	(SEQ ID NO:42),
	TCCATGGCGTTTTTGATGTT	(SEQ ID NO:43),
	TCCATGCCGTTTTTGATGTT	(SEQ ID NO:44),
	TCCATGTCGTTTTTGATGTT	(SEQ ID NO:45),
	TCCATGATGTTTTTGATGTT	(SEQ ID NO:46),
30	TCCATGAAGTTTTTGATGTT	(SEQ ID NO:47),
	TCCATGAGGTTTTTGATGTT	(SEQ ID NO:48),
	TCCATGACATTTTTGATGTT	(SEQ ID NO:49),
	TCCATGACCTTTTTGATGTT	(SEQ ID NO:50),
	TCCATGACTTTTTTGATGTT	(SEQ ID NO:51),
35	TCCATGACGCTTTTGATGTT	(SEQ ID NO:52),
	TCCATGACGATTTTGATGTT	(SEQ ID NO:53),
	TCCATGACGGTTTTTGATGTT	(SEQ ID NO:54),

- 6 -

TCCATGACGTCTTTGATGTT (SEQ ID NO:55),
 TCCATGACGTATTTGATGTT (SEQ ID NO:56), and
 TCCATGACGTGTTTGATGTT (SEQ ID NO:57).

In certain embodiments of the screening methods of the invention, the signal includes
 5 expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway. In one
 embodiment the reporter gene is operatively linked to a promoter sensitive to NF- κ B. In one
 embodiment the signal in response to contacting is binding of the candidate TLR9 ligand or
 CpG DNA to the polypeptide of the invention.

In one embodiment the screening method is performed on a plurality of test
 10 compounds. In one embodiment the response mediated by the TLR9 signal transduction
 pathway is measured quantitatively and the response mediated by the TLR9 signal
 transduction pathway associated with each of the plurality of test compounds is compared
 with a response arising as a result of an interaction between the functional TLR9 and a
 reference immunostimulatory compound.

15

Brief Description of the Figures

Figure 1 depicts a Clustal W multiple sequence alignment of deduced amino acid
 sequences for cat (feline), dog (canine), cow (bovine), mouse (murine), sheep (ovine), pig
 (porcine), horse (equine), human, and rat TLR9 polypeptides. The deduced amino acid
 20 sequences for feline, canine, bovine, murine, ovine, porcine, equine, human, and rat TLR9
 polypeptides shown in the figure correspond to SEQ ID NOs 25, 21, 9, 29, 17, 5, 13, 33, and
 1, respectively. Lines labeled "multiple" refer to the multiple sequence alignment of all six
 sequences shown. Lines labeled "mo/hu" refer to a paired sequence alignment of mouse and
 human TLR9 sequences alone.

25 Figure 2 is a cladogram depicting an evolutionary relatedness tree for rat, murine,
 porcine, bovine, equine, and human TLR9 polypeptides in Figure 1.

Figure 3 is a graph depicting species specificity of TLR9 signaling with selected
 oligonucleotides having strong specificity for human (2006), mouse (5890), or neither (1982).

30

Detailed Description of the Invention

The present invention provides novel amino acid and nucleotide sequences for TLR9
 derived from rat, pig, cow, horse, and sheep. These sequences can be used to identify key
 features of the primary sequences of these and related TLR molecules, including previously

- 7 -

known primary sequences of human and mouse (murine) TLR9. Such key features include binding site information and species specificity toward particular CpG motifs. Native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed *in vitro* or *in vivo* and used in screening assays to identify and to design novel TLR9 ligands.

5 Additionally, the native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed *in vitro* or *in vivo* and used in screening assays to compare various TLR9 ligands, including CpG DNA.

In one aspect the invention provides isolated TLR9 polypeptides, and isolated nucleic acid molecules encoding them, from rat, pig, cow, horse, and sheep. The term "isolated" as
10 used herein with reference to a nucleic acid molecule or polypeptide means substantially free of or separated from components with which it is normally associated in nature, e.g., other nucleic acids, proteins, lipids, carbohydrates or *in vivo* systems to an extent practical and appropriate for its intended use. In particular, the nucleic acids or polypeptides are sufficiently pure and are sufficiently free from other biological constituents of host cells so as
15 to be useful in, for example, producing pharmaceutical preparations. Because an isolated nucleic acid or polypeptide of the invention may be admixed with a pharmaceutically acceptable carrier in a pharmaceutical preparation, the nucleic acid or polypeptide may represent only a small percentage by weight of such a preparation. The nucleic acid or polypeptide is nonetheless substantially pure in that it has been substantially separated from
20 the substances with which it may be associated in living systems.

An amino acid sequence of rat TLR9 is provided as SEQ ID NO:1. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:1 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of rat TLR9 (See
25 Figure 1). Amino acids numbered 1-821 of SEQ ID NO:1 are presumptively extracellular domain and correspond to SEQ ID NO:2. SEQ ID NO:3 is a nucleotide sequence of rat TLR9 cDNA having an open reading frame corresponding to nucleotides 1-3096. SEQ ID NO:4 is a nucleotide sequence of rat cDNA encoding amino acids 1-821 of SEQ ID NO:1.

An amino acid sequence of porcine TLR9 is provided as SEQ ID NO:5. Based on
30 comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:5 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of porcine TLR9

- 8 -

(See Figure 1). Amino acids numbered 1-819 of SEQ ID NO:5 are presumptively extracellular domain and correspond to SEQ ID NO:6. SEQ ID NO:7 is a nucleotide sequence of porcine TLR9 cDNA having an open reading frame corresponding to nucleotides 77-3166. SEQ ID NO:8 is a nucleotide sequence of porcine cDNA encoding amino acids 1-819 of SEQ ID NO:5.

An amino acid sequence of bovine TLR9 is provided as SEQ ID NO:9. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:9 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of bovine TLR9

(See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:9 are presumptively extracellular domain and correspond to SEQ ID NO:10. SEQ ID NO:11 is a nucleotide sequence of bovine TLR9 cDNA having an open reading frame corresponding to nucleotides 84-3170. SEQ ID NO:12 is a nucleotide sequence of bovine cDNA encoding amino acids 1-818 of SEQ ID NO:9.

An amino acid sequence of equine TLR9 is provided as SEQ ID NO:13. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:13 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of equine TLR9 (See Figure 1). Amino acids numbered 1-820 of SEQ ID NO:13 are presumptively extracellular domain and correspond to SEQ ID NO:14. SEQ ID NO:15 is a nucleotide sequence of equine TLR9 cDNA having an open reading frame corresponding to nucleotides 115-3207. SEQ ID NO:16 is a nucleotide sequence of equine cDNA encoding amino acids 1-820 of SEQ ID NO:13.

An amino acid sequence of ovine TLR9 is provided as SEQ ID NO:17. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:17 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of ovine TLR9 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:17 are presumptively extracellular domain and correspond to SEQ ID NO:18. SEQ ID NO:19 is a nucleotide sequence of ovine TLR9 cDNA having an open reading frame corresponding to nucleotides 92-3178. SEQ ID NO:20 is a nucleotide sequence of ovine cDNA encoding amino acids 1-818 of SEQ ID NO:17.

SEQ ID NO:1 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAAEPRSNITSLSLIANRI
HHLHNLDVHLPNVRQLNLKWNCPPLGLSPLHFSCRMTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL
5 SHTNIVLDASSIAGLHSLRVL FMDGNCYKNPCNGAVNVTDAFLGLSNLTHLSLKYNL TEVPRQLPPSLEYL
LLSYNLIVKLGAEEDLANLTSLRMLDVGNCRRCDHAPDLCTECRQKSLDLHPQTFHHLSHLEGLVLKDSLSLSLN
SKWFQGLANLSVLDLSENFLYESINKTSAFQNLTRLRKLDSL FNYCKKVSFARLHLASSFKSLVSLQELNMNGIF
FRLLNKNTLRWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFVDLSNNRISGPPTLSRVAPEKADEAEKGV PW
PASLTPALPSTPVSKNFMVRCKNLRFTMDLSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK
10 VLDLSYNKLDLYHSKSFSELPQLQALDLSYNSQPFMSMQGIGHNFSFLANLSRLQNL SLAHNDIHSRVSSRLYSTS
VEYLD FSGNGVGRMWDEEDLYLYFFQDLRSLIHLDSLQNKHLILRPQNLNYPKSLTKLSFRDNHLSFFNWSSIA
FLPNLRDLDLGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVP AFFALAVELKEVNLSHNILKTVDRSWFGPIV
MNLTVLDVSSNPLHCACGAPFVDLLEVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFGLSLL
AVAVGTVLP LLQHL CGWDVWYCFHLC LAWLPLLTRGRRSAQALPYDAFVVF DKAQSAVADWVYNELRVLEERRG
15 RRALRLCLEDRLWLP GQTLFENLWASTYGSRKTLFVLAHTDKVSGLLRTSFLLAQQRLL LEDRKDVVVLVILRPDA
HRSRYVRLRQRLCRQSVLFWPHQPNGQGSFWAQLSTALTRDNHHFYNRNFCRGPTAE

SEQ ID NO:2 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAAEPRSNITSLSLIANRI
HHLHNLDVHLPNVRQLNLKWNCPPLGLSPLHFSCRMTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL
20 SHTNIVLDASSIAGLHSLRVL FMDGNCYKNPCNGAVNVTDAFLGLSNLTHLSLKYNL TEVPRQLPPSLEYL
LLSYNLIVKLGAEEDLANLTSLRMLDVGNCRRCDHAPDLCTECRQKSLDLHPQTFHHLSHLEGLVLKDSLSLSLN
SKWFQGLANLSVLDLSENFLYESINKTSAFQNLTRLRKLDSL FNYCKKVSFARLHLASSFKSLVSLQELNMNGIF
FRLLNKNTLRWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFVDLSNNRISGPPTLSRVAPEKADEAEKGV PW
25 PASLTPALPSTPVSKNFMVRCKNLRFTMDLSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK
VLDLSYNKLDLYHSKSFSELPQLQALDLSYNSQPFMSMQGIGHNFSFLANLSRLQNL SLAHNDIHSRVSSRLYSTS
VEYLD FSGNGVGRMWDEEDLYLYFFQDLRSLIHLDSLQNKHLILRPQNLNYPKSLTKLSFRDNHLSFFNWSSIA
FLPNLRDLDLGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVP AFFALAVELKEVNLSHNILKTVDRSWFGPIV
MNLTVLDVSSNPLHCACGAPFVDLLEVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFG
30

SEQ ID NO:3 (Rat TLR9)

atgggttctctgtcgcaggaccctgcaccccttgtctctcctggtacaggccgcagtgctggctgaggctctggcc
ctgggtacctgcctgccttctacccctgtgaactgaagcctcatggcctggtagactgcaactggctcttctctg
aagtctgtgcctcacttctctgcccgcagaaccccggtccaacatcaccagccttctcttgatcgccaaccgcac
35 caccacctgcacaacctgcacttctgcccactgcccacagtgccagcagctgaacctcaagtggaaactgtccgccc
cctggcctcagccccttgcaacttctcctgcccgcagcaccattgagcccaaaccttctggctatgcgcatgctg
gaagagctgaacctgagctataacgggtatcaccactgtgccccgcctgccagctccctgacgaatctgagccta
agccacaccaacatcctggtactcgatgccagcagcctcgctggcctgcacagcctgcagattctcttcatggac
gggaactgctactacaagaacccctgcaacggggcggtgaacgtgaccccgagccttctctgggcttgagcaac
40 ctacccacttgtcccttaagtataacaacctcacagaggtgccccgccaactgccccccagcctggagtacctc
ctgctgtctataacctcatcgtcaagctgggggcgaagacctagccaacctgacctcccttcgaatgcttgat
gtgggtgggaattgcctgctgtgatcacgccccgacctctgtacagaatgccggcagaagctcccttgatctg
caccctcagacttccatcacctgagccacctggaaggcgtggtgctgaaggacagttctctcactcgctgaac
tccaagtgggtccagggtctggcgaaacctctcggtgctggacctaagcgagaacttctctacgagagcatcaac
45 aaaaccagcgcttccagaacctgacctgctgcgaagctcgacctgtccttcaattactgcaagaaggtatcg
ttcgcccgctccacctggcaagttccttcaagagcctgggtgctgctgcaggagctgaacatgaacggcatcttc
ttcgcttactcaacaagaacacgctcaggtggctggctggtctgcccagctccacacgctgcaccttcaaatg
aatctcatcaaccaggcgagctcagcgtctttagtacctcccgagcccttcgcttctgtggacctgtccaataat
cgcacagcgggctccaacgctgtccagagctgccccgaaaaggcagacgaggcgagagggttccatgg
50 cctgcaagtctcaccctcagctctcccgagcactccgctctcaagaacttcatggctcaggtgtaagaacctcaga
ttcaccatggactgtctcggaacaaccaggtgactatcaagccagagatgttcgtcaaccttccatctccag
tgtctgagctgagccacaactgcatcgcgaggctgtcaatggctctcagttctctgcccgtgaccaacctgaag
gtgctggacctgtcctataacaagctggacctgtaccattcgaaatcgttcagtgagctcccacagttgcaggcc

- 10 -

ctggacctgagctacaacagccagccattcagcatgcaggggatagccacaacttcagttttctggccaatctg
tccaggttacagaaccttagcctggcacacaatgacattcacagccgctgtcctcacgcctctacagcacctca
gtggagtatctggacttcagcggcaacgggtgtgggcccagcatgtgggacgaggaggacctttacctctatttcttc
caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggccccagaacctcaac
5 tacctccccaagagcctgacgaagctgagttccgtgacaatcacctctctttctttaactggagcagctctggcc
ttcctgccaatctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcaccctgccta
ggcagctcctccagaaactggatgtcagtagcaacagtatcgtctttgtgggtcccagcctctcttgccttggcg
gtagagctaaaagaggtcaacctcagccataacatcctcaagactgtggatcgctcctgggttggggccattgtg
atgaacctgacgggtctagacgtgagcagcaacctctgcattgtgcctgcggtgcacccttctgagacttactg
10 ctggaagtgcagaccaaggtgcctggcctggctaaccggtgtgaagtgtggcagctcccggccagctgcagggccgc
agcatctttgcgaagacctgcggctgtgcctggatgacgtcctttctcgggactgcttggcctttcactcctg
gctgtggcctgggacacggtgtgcctttactgcagcatctctcgggctgggacgtctggtagctgttccatctg
tgcctggcatggctacctttgtgacctgtggcggcgacgcgccaagctctccttatgatgccttcgtgggtg
ttcgataaggcgacagagcggttgcctgactgggtgtataacagacttcgagtgcggttagaggagcggcgcggt
15 cgccgagccctacgcttgtgtctggaggacagattggctgcctggccagacactcttcgagaacctctggggcc
tccatcttggcagcgcaagactctgtttgtgctggccacacgagcaaggtcagtgccctcctgcgcaccagc
ttcctgctggctcagcagcgctgctggaggaccgcaaggacgtggtggtgttggtgatcctgcgcctgatgcc
caccgctcccgctacgtgcgactgcgccagcgctctgcgcgacagtggtgctcttctggccccatcagcccaac
gggcagggcagcttctggggccagctgagtacagccctgactagggacaaccaccacttctataaccggaacttc
20 tgcgggggacctacagcagaatag

SEQ ID NO:4 (Rat TLR9)

atgggtctctgtcgcaggacctgcaccccttgtctctcctggtagcaggccgagtgctggctgaggtcttggcc
ctgggtacctgctgcttctcctaccctgtgaactgaagcctcatggcctggtagactgcaactggctcttctctg
25 aagtctgtgctcacttctctgcccagacaacccggttcccaactcaccagccttctcttgatcgccaaccgcata
caccacctgcacaacctcgacttctgcacctgcccacagctgcagcagctgaacctcaagtggaactgtccgccc
cctggcctcagcccttgcacttctcctgcccagatgaccattgagcccaaaccttctggctatgcgcagctg
gaagagctgaacctgagctataacggtatcaccactgtgccccgctgcccagctcctgacgaatctgagccta
agccacaccaacatcctggtactcgatgccagcagcctcgctggcctgcacagcctgcgagttctcttcatggac
30 gggaactgctactacaagaacccctgcaacggggcggtgaacgtgaccccgagccttctcctgggcttgagcaac
ctcaccaccttgtcccttaagtataacaacctcacagaggtgccccgccaactgccccccagcctggagtacctc
ctgctgtcctataacctcatcgtcaagctgggggcccgaagacctagccaacctgacctccttctggaatgctgat
gtgggtgggaattgcgctcgctgtgatcagcgcctccgacctctgtacagaatgcccggcagaagtccttctgatctg
caccctcagacttccatcacctgagccacctgaaggcctgggtgctgaaggacagttctctcactcgctgaac
35 tccaagtgggtccagggtctggcgaaacctctcggtgctggacctaaagcgagaacttctctacgagagcatcaac
aaaaccagcgcttctcagaacctgacctgtgctgcgaagctcgacctgtccttcaattactgcaagaaggatctg
ttcgcccgctccacctggcaagttccttcaagagcctgggtgtcgctgcaggagctgaacatgaacggcatcttc
ttcgcttactcaacaagaacacgctcaggtggctggctggctgtgcccaagctccacacgctgcaccttcaaatg
aatttcatcaaccaggcgagctcagcgtctttagtacctccgagcccttcgcttctgtggacctgtccaataat
40 cgcacagcgggctccaacgctgtccagagtcgccccgaaaaggcagacgaggcgagaaagggttccatgg
cctgcaagctctaccccgactctcccgagcactccgctctcaaagaacttcatggctcaggtgtaagaacctcaga
ttcaccatggacctgtctcggaacaaccaggtgactatcaagccagagatgttcgtcaacctctccatctccag
tgtctgagcctgagccacaactgcatcgcgaggctgtcaatggctctcagttcctgcccgtgaccaacctgaag
gtgtggacctgtctataacaagctggacctgtaccattcgaaatcgttcagtgagctccacagttgcaggcc
45 ctggacctgagctacaacagccagccattcagcatgcaggggatagggccacaacttcagttttctggccaatctg
tccaggttacagaaccttagcctggcacacaatgacattcacagccgctgtcctcacgcctctacagcacctca
gtggagtattctgacttcagcggcaacggtgtggtggccgcatgtgggacgaggaggaccttacctctatttcttc
caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggccccagaaacctcaac
tacctcccaagagcctgacgaagctgagtttccgtgacaatcacctctcttctttaaactggagcagctctggcc
50 ttctgccccaatctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcaccctgccta
ggcagctcctccagaaactggatgtcagtagcaacagtatcgtctttgtgggtcccagccttcttctgtctggcg
gtagagctaaaagaggtcaacctcagccataacatcctcaagactgtggatcgctcctgggttggggccattgtg
atgaacctgacgggtctagacgtgagcagcaacctctgcattgtgcctgcgggtgcacccttctgtagacttactg
ctggaagtgcagaccaaggtgcctggcctggctaaccggtgtgaagtgtggcagctcccggccagctgcaggggccg
55 agcatcttctgcgcaagacctgcggctgtgcctggatgacgtccttctcgggactgcttggc

- 11 -

SEQ ID NO:5 (Porcine TLR9)

MGPRCTLHPLSLLVQVLTALAAALAQGRLPAPFLPCELPQPHGLVNCNWFLKSVPHFSAAAPRANVTSLSLLSNRIH
HLHDSDFVHLSSLRTLNLKWNCPAGLSPMHFPCMTIEPNTFLAVPTLEELNLSYNSITTVPALPDSLVSLSLS
RTNIIIVLDPTHLTGLHALRYLYMDGNCYKNPCQGALEVVPGALLGLGNLTHLSLKYNNTTEVPRSLPPSLETLL
5 LSYNHIVTLTPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKDHPLHSDTFSHLSRLEGLVLKDSLYNLDT
RWFRLDRLQVLDLSENFLYDCITKTTAFQGLARLSLNLNFYHKKVSFAHLHLAPSFGLHLSRLEKELDMHGIF
RSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFFGLLYVDLSDNRISGAARPVAITREVDGRERVWLPSR
NLAPRPLDTRLSEDMPNCKAFSFTLDLSRNNLVTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVL
10 DLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMTQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSQQQLCSASLC
ALDFSGNDLSRMWAEGLYLRFFQGLRSLVWLDLSQNLHLLTLLPRALDNLPKSLKHLHLRDNNAFFNWSSLTLL
PKLETLDLAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFGSMVGN
LKVLVDVSANPLHCACGATFVGFLLEVQAAVPGPLSRVKCGSPGQLQGHISIFAQDLRLCLDETLSWNCFLISLLAM
ALGLVVPMLHHLGWDLWYCFHLCLAWLPHRGQRRGADALFYDAFVVFDKAQSAVADWVYNELRVQLEERRGRRA
15 LRLCLEERDWWLPGKTLFENLWASVYSSRKTFLVLAHTDRVSGLLRASFLLAQQRLLDRKDVVVLVILRPDAYRS
RYVRLRQRLCRQSVLLWPHQPRGQGSFWAQLGTALTRDNHFFYNRNFCRGPTTAE

SEQ ID NO:6 (Porcine TLR9)

MGPRCTLHPLSLLVQVLTALAAALAQGRLPAPFLPCELPQPHGLVNCNWFLKSVPHFSAAAPRANVTSLSLLSNRIH
HLHDSDFVHLSSLRTLNLKWNCPAGLSPMHFPCMTIEPNTFLAVPTLEELNLSYNSITTVPALPDSLVSLSLS
20 RTNIIIVLDPTHLTGLHALRYLYMDGNCYKNPCQGALEVVPGALLGLGNLTHLSLKYNNTTEVPRSLPPSLETLL
LSYNHIVTLTPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKDHPLHSDTFSHLSRLEGLVLKDSLYNLDT
RWFRLDRLQVLDLSENFLYDCITKTTAFQGLARLSLNLNFYHKKVSFAHLHLAPSFGLHLSRLEKELDMHGIF
RSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFFGLLYVDLSDNRISGAARPVAITREVDGRERVWLPSR
NLAPRPLDTRLSEDMPNCKAFSFTLDLSRNNLVTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVL
25 DLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMTQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSQQQLCSASLC
ALDFSGNDLSRMWAEGLYLRFFQGLRSLVWLDLSQNLHLLTLLPRALDNLPKSLKHLHLRDNNAFFNWSSLTLL
PKLETLDLAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFGSMVGN
LKVLVDVSANPLHCACGATFVGFLLEVQAAVPGPLSRVKCGSPGQLQGHISIFAQDLRLCLDETLSWNCFLISLLAM

30 SEQ ID NO:7 (Porcine TLR9)

gagcacgaacatccttcaactgtagctgctgcccgtctgccagccagaccctttggagaagacccccactccctgt
catgggcccccgctgcacccctgcacccctttctctcctgggtgcaggtgacagcgctggctgcggctctggccca
gggcaggtgcctgccttctgcccctgtgagctccagccccacggcctggtgaactgcaactggctcttctgaa
gtccgtgccccacttctcgccgagcgcgcgcgggccaacgtcaccagcctctccttactctccaaccgcatcca
35 ccacctgcacgactccgacttcgtccacctgtccagcctacgaactctcaacctcaagtggaaactgcccgcggc
tggcctcagccccatgcacttccccctgccacatgaccatcgagcccaacaccttccctggcctgcccaccctgga
ggagctgaacctgagctacaacagcatcacgacctgacctgcccactccctcgtgtccctgtcgctgag
ccgcaccaacatcctggtgctagacccacccacctcactggcctacatgccctgcgctacctgtacatggatgg
caactgctactacaagaacccctgccagggggcgctggagggtgctcggggtgcccctcctcgccctgggcaacct
40 cacacatctctcactcaagtaacaacaatctcacggaggtgccccgcagcctgccccccagcctggagacctgct
gttgctctacaaccacattgtcacccctgacgctgaggacctggccaatctgactgcccctgcgctgcttgatgt
gggggggaactgcccgcgtgtgacctgcccgaacccctgcagggagtgcccaaggaccaccccaagctgca
ctctgacaccttcagccacctgagcgcctcgaaaggcctggtgttgaaagacagttctcttacaacctggacac
caggtggttccgaggcctggacaggtctcaagtctggacctgagtgagaacttccctctacgactgcatcaccaa
45 gaccacggccttccaggcctggccgactgcgcagcctcaacctgtccttcaattaccacaagaaggtgtcctt
tgcccactgcacctggcaccctcctttgggcacctccggtccctgaaggagctggacatgcatggcatcttctt
ccgctcgctcagtgagaccacgctccaacctctggtccaactgcctatgctccagaccctgcgctgcagatgaa
cttcattaaccaggccagctcagcatcttggggccttccctggcctgctgtacgtggacctatcggaacaaccg
catcagcggagctgcaaggccagtgccattactaggagggtggatggtaggagagggtctggctgccttccag
50 gaacctcgctccacgtccactggacactctccgctcagaggacttcatgccaaactgcaaggccttcagcttcac
cttgagacctgtctcggaacaacctgggtgacaatccagtcggagatgtttgctcgccctctcacgctcgagtgcct
gcgctgagccacaacagcatctcccaggcgtcaatggctctcagtttgtgcgctgaccagcctgcgggtgct
ggacctgtcccacaacaagctggacctgtatcacgggcgtcgttcacggagctgcccgcctgggaagcactgga
cctcagctacaatagccagccctttaccatgcagggtgtggggccacaacctcagcttcgtggccagctgcccgc

- 12 -

cctgcgctacctcagcctggcgcaaatgacatccatagccgagtgtcccagcagctctgtagcgcctcactgtg
cgccctggacttttagcggcaacgatctgagccggatgtgggctgagggagacctctatctccgcttcttccaagg
cctaagaagccttagtctggctggacctgtcccagaaccacctgcacaccctcctgccacgtgccctggacaacct
ccccaaaagcctgaagcatctgcatctccgtgacaataacctggccttcttcaactggagcagcctgaccctcct
5 gcccagctggaaacctggacttggctggaaaccagctgaaggccctaagcaatggcagcctgccatctggcac
ccagctgcggaggctggacctcagtggaacacagcatcggcttctgtgaacctggcttcttggcctggccaagca
gttagaagagctcaacctcagcgccaatgccctcaagacagtggaagccctcctggtttggtcgtatggtgggcaa
cctgaaagtccctagacgtgagcgccaacctctgcaactgtgcctgtggggcgaccttcgtgggcttctgtgga
ggtacaggctgcgctgacctgggctgccagcccgctcaagtgtggcagtcggggcgacctccagggccatagcat
10 ctttgcgcaagacctgcgctctgcctggatgagacctctcgtggaactgttttggtatctcgtgctggccat
ggcctgggctgggttgtgcccattgctgcaccacctctgcggctgggacctctggtactgcttccacctgtgcct
ggcctggctgccccaccgagggcagcgggcgggcgagacgcctgttctatgatgccttcgtggcttcttgacaa
agctcagagtgtgtggccgactgggtgtacaacgagctgccccgtgcagctggaggagcgccgtggcgccgccc
actgcgctgtgcctggaggagcgagactggttacctggcaagacgctcttcgagaacctgtgggacctcagtcta
15 cagcagcgcaagacctgttctgtgctggccacacggacctgtcagcgccctcttgcgtgccagtttctgtgct
ggcccagcagcgctgtggaggacgcaaggacgttgtagtgtggtgatcctgcgccccgatgcctaccgctc
ccgctacgtgcggctgcccagcgctctgcgccagagtgtcctcctctggccccaccagccccgtggcgagg
cagcttctgggcccagctgggcacagccctgaccagggacaaccaccttctataaccggaactctgcgggg
ccccacgacagccgaatagcactgagtacagccagttgccccagccccctggatttgcctctctgcctgggg
20 tgcccaacctgcttctgctcagccacacctgctctgctcctgttccccacccccccccccagcctggcatgt
aacatgtgccaataaatgtaccggaggggccaagaaaaaaaaaaaaaaaaa

SEQ ID NO:8 (Porcine TLR9)

atgggcccccgctgcaccctgcaccccccttctctcctgggtgcaggtgacagcgctggctgcggctctggccag
25 ggcaggctgcctgccttctgcctgtgagctccagccccacggcctgggtgaactgcaactggctcttctgaag
tcctgccccacttctcggcgccagcgccccggccaacgtcaccagcctctccttactctccaaccgcatccac
cacctgcacgactccgacttctgctccacctgtccagcctacgaactctcaacctcaagtggaaactgcccccggt
ggcctcagccccatgcacttccccctgccacatgaccatcgagcccaacaccttccctggccgtgccaccctggag
gagctgaacctgagctacaacagcatcacgaccgtgcctgcctgcgcgactccctcgtgtccctgtcgtgagc
30 cgcaccaacatcctgggtgctagacccccaccacctcactggcctacatgcctgcgctacctgtacatggatggc
aactgctactacaagaaccttgcagggggcgctggagggtggtgccccgtgcctcctcggcctgggcaacctc
acacatctctcactcaagtacaacaatctcacggagggtgccccgcagcctgccccccagcctggagacctgctg
ttgtcctacaaccacattgtcacctgacgctgaggacctggccaatctgactgcctgcgctgcttgatgtg
ggggggaactgcgcccgtgtgacctgcccgaaccttgcagggagtgcctaaaggaccaccccaagctgcac
35 tctgacaccttcagccacctgagccgctcgaaggcctgggtgttgaaagacagttctctctacaacctggacacc
aggtggttccgaggcctggacaggtcccaagtgtggacctgagtgagaacttctctacgactgcatcaccaag
accacggccttccagggcctggccgactgcgcagcctcaacctgtccttcaattaccacaagaaggtgtcctt
gcccacctgcacctggcacctccttgggacacctcgggtcctgaaggagctggacatgcatggcatctcttcc
cgctcgctcagtgagaccacgctccaacctctggtccaactgcctatgctccagacctgcgctgcagatgaac
40 ttcatataaccaggccagctcagcatcttggggccttccctggcctgctgtacgtggacctatcggaacaaccg
atcagcggagctgcaaggccagtgccattactaggagggtggatggtagggagagggtctggctgccttccagg
aacctcgctccacgtccactggacactctccgctcagaggacttcattgccaactgcaaggccttcagcttcacc
ttggacctgtctcggaacaacctgggtgacaatccagtcggagatgttgcctgcctctcacgcctcagtgccctg
cgctgagccacaacagcatctccaggcggtcaatggctctcagtttgtgcccgtgaccagcctgcgggtgctg
45 gacctgtcccacaacaagctggacctgtatcacggcgctcgttcacggagctgcccgcctggaagcactggac
ctcagctacaatagccagccttaccatgcagggtgtggggccacaacctcagcttctgaggccagctgcccgc
ctgcgctacctcagcctggcgcaaatgacatccatagccgagtgctccagcagctctgtagcgctcactgtgc
gacctggacttttagcggcaacgatctgagccggatgtgggctgagggagacctctatctccgcttcttccaaggc
ctaagaagcctagtctggctggacctgtcccagaaccacctgcacacctcctgccacgtgccctggacaacctc
50 cccaaaagcctgaagcatctgcatctccgtgacaataacctggccttcttcaactggagcagcctgacctcctg
cccaagctggaaacctggacttggctggaaaccagctgaaggccctaagcaatggcagcctgccatctggcacc
cagctgcggaggctggacctcagtggaacacagcatcggcttctgtgaacctggcttcttggcctggccaagcag
ttagaagagctcaacctcagcgccaatgccctcaagacagtggaagccctcctggtttggtcgtatggtgggcaac
ctgaaagtccagcgtgagcgccaacctctgcatctgctgctgtggggcgaccttcgtgggcttctgctggag
55 gtacaggctgcgctgctgggctgccagcccgctcaagtgtggcagtcggggcgagctccagggccatagcatc
tttgcgcaagacctgcgctctgcctggatgagacctctcgtggaactgttttggc

- 13 -

SEQ ID NO:9 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGLPAFLPCELPQPHGQVDCNWLFLKSVPHFSAGAPRANVTSLSLISNRIH
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSSLVSLSL
5 HTSILVLGPTHFTGLHALRFLYMDGNCYMNPCCPRALEVAPGALLGLGNLTHLSLKYNNTLTPRRPLPSLDTLL
LSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPLHPDTFSHLSRLEGLVLKDSLSLYKLEK
DWFRGLGRLQVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNYHKKVSFAHLHLASSFGSLVSLEKLDMHGIF
RSLTNITLQSLTRLPKLQSLHLQLNFINQAQLSIFGAFPSLLFVDLSDNRISGAATPAAALGEVDSRVEVWRLPR
GLAPGPLDAVSSKDFMPSCNLFNFTLDSRNMLVTIQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD
10 LSHNKLDLYHGSRFTLQLEALDLSYNSQPFMSQGVGHNLSFVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLNLPKSLRQLRLRDNNLAFFNWSSTVLP
RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVPIPGFFVRATRLIELNLSANALKTVDPSWFGSLAGTL
KILDVSANPLHCACGAADFVDFLLERQEAHPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLSDCFGLSLLMVA
LGLAVPMLHHLGCWDLWYCFHLCLAHLPRRRRRQGEDTLLYDAVVVFDKVQSAVADWVYNELRVQLEERRGRRAL
15 RLCLEERDNLPGKTLFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLAQORLLEDKDVVVLVILRPAAYRSR
YVRLRQRLCRQSVLLWPHQPSGQGSFWANLGIALTRDNRHFYNRNFCRGPTTAE

SEQ ID NO:10 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGLPAFLPCELPQPHGQVDCNWLFLKSVPHFSAGAPRANVTSLSLISNRIH
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSSLVSLSL
20 HTSILVLGPTHFTGLHALRFLYMDGNCYMNPCCPRALEVAPGALLGLGNLTHLSLKYNNTLTPRRPLPSLDTLL
LSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPLHPDTFSHLSRLEGLVLKDSLSLYKLEK
DWFRGLGRLQVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNYHKKVSFAHLHLASSFGSLVSLEKLDMHGIF
RSLTNITLQSLTRLPKLQSLHLQLNFINQAQLSIFGAFPSLLFVDLSDNRISGAATPAAALGEVDSRVEVWRLPR
GLAPGPLDAVSSKDFMPSCNLFNFTLDSRNMLVTIQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD
25 LSHNKLDLYHGSRFTLQLEALDLSYNSQPFMSQGVGHNLSFVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLNLPKSLRQLRLRDNNLAFFNWSSTVLP
RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVPIPGFFVRATRLIELNLSANALKTVDPSWFGSLAGTL
KILDVSANPLHCACGAADFVDFLLERQEAHPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLSDCFGLSLLMVA
30

SEQ ID NO:11 (Bovine TLR9)

gggaagtggggcgccaagcacccttccctgcagctgcctcccaacctgcccgcagaccctctggagaagccgcat
tccctgtcatgggcccctactgtgccccgcaccccccttctctcctggtgcaggcgggcgccactggcagcgggccc
tggcggagggcgaccctgectgccttccctgcccgtgtgagctccagcccatgggtcaggtggactgcaactggctgt
35 tccctgaagtctgtgcccgcacttttcggctggagcccccgggccaatgtcaccagcctctccttaatctccaacc
gcatccaccacttgcatgactctgacttcgtccacctgtccaacctgcccgtcctcaacctcaagtggaaactgcc
cgccggcgccgctcagccccatgcacttccctgcccgtatgaccatcgagcccaacacacttccctggctgtgccca
ccctggaggagctgaacctgagctacaacggcatcacgaccgtgcctgcccagttccctcgctgtccctgt
cgctgagccacaccagcatcctggtgctaggccccaccacttcaccggcctgcacgcccctgcgcttctgtaca
40 tggacggcaactgctactacatgaaccctgcccgcgggcccctggaggtggccccagggcctcctcgccctgg
gcaacctcacgcacctgtcgctcaagtacaacaacctcacggaggtgccccgcgcccctgccccagcctggaca
ccctgtgctgtcctacaaccacattgtcaccctggcaccggaggaacctggccaacctgactgcctgcccgtgc
ttgacgtgggtgggaactgcccgcgctgcgacctgcccgaaccctgcagggagtgcccaagaacttcccca
agctgcaccctgacaccttcagtcacctgagcgccctcgaaggcctggtgttgaggagacttctctctacaaac
45 tagagaaagattggttccgcccctggcgaggctccaagtgcctgacctgagtgagaactcctctatgactaca
tcaccaagaccacatcttcaacgacctgaccagctgcgcagactcaacctgtccttcaattaccacaagaagg
tgtccttcgcccacctgcacctagcgtcctccttgggagctgtggtgtccctggagaagctggacatgcacggca
tcttcttcgctccctcaccacatcacgctccagtcgctgaccggctgcccagctccagagctgtcatctgc
agctgaacttcatcaaccaggcccagctcagcatcttggggccttcccagagcctgctctcgtggacctgtcgg
50 acaaccgcatcagcggagccgcgacgcccagcggcgccctgggggaggtggacagcaggggtggaagtctggcgat
tgcccaggggcccctcgctccaggcccgtggacgcccgtcagctcaaaggacttcatgccaagctgcaacctcaact
tcacctggacctgtcacggaacaacctgggtgacaatccagcaagagatgtttaccgcccctctccgcccctcag
gcctgcgcccgtgagccacaacagcatctcgaggcggttaatggctcccagttcgtgcccgtgaccagcctgcgag

- 14 -

tgctcgacctgtcccacaacaagctggacctgtaccatgggcgctcattcacggagctgccgcagctggaggcac
tggaacctcagctacaacagccagcccttcagcatgacgggctgggcccacaacctcagcttcgtggcccagctgc
cctccctgcgctacctcagccttgccgacaaatggcatccacagccgctgtcacagaagctcagcagcgctcgt
5 tgcgcgcccctggacttcagcggcaactccctgagccagatgtgggcccaggagacctctatctctgcttttca
aaggcttgaggaacctgggtccagctggacctgtccgagaacctctgcacacctcctgcctcgtcacctggaca
acctgcccagagcctgcccgcagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgaccg
tcttgcctccgctggaagccctggatctggcaggaaccagctgaaggccctgagcaacggcagcctgcccgcctg
gcatccggctccagaagctggagctgagcagcaacagcatcggttcgtgatccccggcttcttctgctccgcgga
10 ctcggtgatagagcttaacctcagcgccaatgcccctgaagacagtggatccctcctgggttcgggttcttagcag
ggacctgaaaatcctagacgtgagcgccaaccgctccactgcgctgcccggggcgcccttcttggttcttgcg
tgagagacagggagccgtgcccgggctgtccaggcgcgctcacatgtggcagtcggggccagctccagccgca
gcatcttcacacaggaacctgcgctctgctggatgagacctctccttggtactgcttggcctctcactgctaa
tggtggcgctgggctggcagtgcccatgctgcaccacctctgtggctgggacctctggtactgcttccacctgt
15 gtctggcccttggcccgcagggcgccgagcggggcgaggacacctgctctatgatgccgtcgtggtcttcg
acaaggtgcagagtgcagtggtgattgggtgtacaacgagctccgctgagctggaggagcgccggggcgcc
ggcgctccgctctgctggaggagcgagactggctccctggtaagacgctcttcgagaacctgtgggctcgg
tctacagcagccgaagacctgttctgctggaccacacgggagccgggtcagcgccctcctgcgcccagcttcc
tgctggcccagcagcgctgttgaggagccgaaggagctcgtagtgtggtgatcctgcgcccagcctatc
20 ggtcccgctacgtgcggctgcgccaagcgctctgcccagagcgctcctccttgccccaccagccagtggtcc
agggtagtttctgggccaacctgggcatagccctgaccagggaaccgtcacttctataaccggaaacttctgcc
ggggcccccacgacagccgaatagcacagagtgaactgcccag

SEQ ID NO:12 (Bovine TLR9)

atggggccctactgtgccccgcaccccttctctcctgggtgagggcgccggaactggcagcgccctggccgag
25 ggcacctgcctgccttccgtgctgagctccagcccatgggtcaggtggactgcaactggctgttctgaag
tctgtgcccgaacttttccggctggagcccccgggccaatgtcaccagcctctccttaacttccaaccgcatccac
cacttgcatgactctgacttctgtccacctgtccaacctgcgggtcctcaacctcaagtggaaactgccgcggcc
ggcctcagccccatgcacttcccctgcccgtatgaccatcgagcccaacaccttccctggctgtgcccacctggag
30 gagctgaacctgagctacaacggcatcacgacctgcctgcccctgcccagttccctcgtgtccctgtcgctgagc
cacaccagcatcctgggtgctagggccccaccacttcacggcctgcacgcccctgcgcttctgtacatggacggc
aactgtactacatgaacccctgcccgcgggcccctggaggtggccccagggcgcctcctcggcctgggcaacctc
acgcacctgtcgctcaagtacaacaacctcacggaggtgccccgcgctgccccccagcctggacacctgctg
ctgtcctacaaccacattgtcacctggcaccgaggacctggccaacctgactgcccctgcgctgcttgacgtg
35 ggtgggaactgcccgcgctgcgacctgcccgaacccctgcaggagtgcccaagaacttccccagctgcac
cctgacaccttcagtcacctgagccgctcgaaggcctgggtgtgaaggacagttctctctacaaactagagaaa
gattgggtccgcccctgggcaggtccaagtgtcgacctgagtgagaacttctctatgactacatcaccaag
accacctcttcaacgacctgaccagctgcgcagactcaacctgtccttcaattaccacaagaaggtgtccttc
40 gccacctgcacctagcgtcctccttggagtgctgggtgtccctggagaagctggacatgcacggcatcttcttc
cgctccctcaccaacatcacgctccagtcgctgaccggctgcccagctccagagctgcatctgcagctgaac
ttcatcaaccaggcccagctcagcatcttggggccttcccagcctgctctcctggtgacctgtcggacaaccgc
atcagcggagccgcgacgcccagcgccgctgggggaggtggacagcaggggtggaagtctggcgattgcccagg
ggcctcgctccaggcccgtggacgcccgtcagctcaaaggacttcatgccaagctgcaacctcaacttcaccttg
gacctgtcacggaacaacctgggtgacaatccagcaagagatgtttaccgcctctccgcctccagtgctgcgc
45 ctgagccacaacagcatctgcaggcggttaatgggtcccagttcgtgcccgtgaccagcctgagagtgctcgac
ctgtcccacaacaagctggacctgtaccatgggcgctcattcacggagctgcccagctggaggcactggacctc
agctacaacagccagcccttcagcatgcaggcgctggggccacaacctcagcttctggtggccagctgcccctcctg
cgctacctcagccttgccgacaaatggcatccacagccgctgtcacagaagctcagcagcgccctggtgcgccc
ctggacttcagcggcaactccctgagccagatgtgggcccaggaggacctctatctctgcttttcaaggcttg
50 aggaacctgggtccagctggacctgtccgagaacctctgcacacctcctgcctcgtcacctggacaacctgccc
aagagcctgcccagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgacctcctgccc
cgctggagccctggatctggcaggaaccagctgaaggccctgagcaacggcagcctgcccgcctggcatccgg
ctccagaagctggagctgagcagcaacagcatcggtctcgtgatccccggcttcttctgctccgcggaactcggtg
atagagcttaacctcagcgccaatgcccgaagacagtggtacccctcctggttcggttcttagcaggagacctg
55 aaaatcctagacgtgagcgccaaccgctccactgcgctgcccggggcgcccttgggtgacttctgagagaga
caggaggccgtgcccgggctgtccaggcgctcacatgtggcagtcggggccagctccaggggcgagcatcttc
acacaggacctgcgctctgctggatgagacctctccttggtgactgcttggc

- 15 -

SEQ ID NO:13 (Equine TLR9)

MGPCHGALQPLSLLVQAAMLAVALAQGTLPFFLPCELQPHGLVNCNWLFLKSVPHFSAAPRDNVTSLSLLSNRI
 HHLHDSDFQLSNLQKLNKWNCPAGLSPMHFPCMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLIL
 5 SRTNQLDPTSLTGLHALRFLYMDGNCYKNPCGRALEVAPGALLGLGNLTHLSLKYNLTTPVPSLPSSLEYL
 LLSYNHIVTLAPEDLANLTALRVLDVGGNCRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSLSLYQLN
 PRWFRGLGNLTVDLSENFLYDCITKTAKFQGLAQLRRLNLSFNYHKKVSFAHLTLAPSFGLSLSLQELDMHGIF
 FRSLSQKTLQPLARLPMLQRLYLQMNFINQAQLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGGKKVWLTS
 RDLTPGPLDTPSSEDFMPSCKNLSFTLDLSRNNLVTVQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV
 10 LDLSHNKLDLYHGRSFTLPRLEALDLSYNSQPFSSMRGVGHNLFSVAQLPTLRYLSLAHNGIHSRVSQQLCSTSL
 WALDFSGNSLSQMWAEGLDLYLRFFQGLRSLIRLDLSQNLRLHTLLPCTLGNLPKSLQLLRLRNNYLAFFNWSSLTL
 LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRNSIIFVVPGFALATRLRELNLSANALRTEEPSWFGFLAG
 SLEVLVDVSANPLHCACGAAFVDFLLQVQAAVPGLPSPRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFGLSLLV
 VALGLAMPMLHHLGWDLWYCFHLGLAWLPRRGWQRGADALSYPVDFDKAQSADWVYNELRVRLERERRRR
 15 ALRLCLEERDWPGLKTLFENLWASVYSSRKMFLVLAHTDQVSGLLRASFLLAQORLLEDKRDVVLVILSPDARR
 SRYVRLRQRLCRQSVLFWPHQPSGQRSFWAQLGMALTRDNRHFYNQNFRCGPTMAE

SEQ ID NO:14 (Equine TLR9)

MGPCHGALQPLSLLVQAAMLAVALAQGTLPFFLPCELQPHGLVNCNWLFLKSVPHFSAAPRDNVTSLSLLSNRI
 HHLHDSDFQLSNLQKLNKWNCPAGLSPMHFPCMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLIL
 20 SRTNQLDPTSLTGLHALRFLYMDGNCYKNPCGRALEVAPGALLGLGNLTHLSLKYNLTTPVPSLPSSLEYL
 LLSYNHIVTLAPEDLANLTALRVLDVGGNCRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSLSLYQLN
 PRWFRGLGNLTVDLSENFLYDCITKTAKFQGLAQLRRLNLSFNYHKKVSFAHLTLAPSFGLSLSLQELDMHGIF
 FRSLSQKTLQPLARLPMLQRLYLQMNFINQAQLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGGKKVWLTS
 25 RDLTPGPLDTPSSEDFMPSCKNLSFTLDLSRNNLVTVQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV
 LDLSHNKLDLYHGRSFTLPRLEALDLSYNSQPFSSMRGVGHNLFSVAQLPTLRYLSLAHNGIHSRVSQQLCSTSL
 WALDFSGNSLSQMWAEGLDLYLRFFQGLRSLIRLDLSQNLRLHTLLPCTLGNLPKSLQLLRLRNNYLAFFNWSSLTL
 LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRNSIIFVVPGFALATRLRELNLSANALRTEEPSWFGFLAG
 SLEVLVDVSANPLHCACGAAFVDFLLQVQAAVPGLPSPRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFG
 30

SEQ ID NO:15 (Equine TLR9)

ctctgttctctgagctgttgccgctgaagggactgagcagacaaagcatcctcctctgcagctgctgccagtg
 tgccagctggaccctctggatcatctcccactccctgtcatgggccccttgccatggtgcccctgcagcccctgtct
 ctctggtgagcgccatgctggcctggtcttgcccaaggcaccctgcctcccttccctgcccctgtgagctc
 35 cagccccacggcctggtgaactgcaactggctgttccctgaagtccgtgccccacttctcagcagcagcaccgccg
 gacaatgtcaccagccttccctgtctccaaccgcatccaccacctccagcactccgactttgcccactgtcc
 aacctgcagaaactcaacctcaaatggaactgcccgcagcggcctcagccccatgcacttcccctgccacatg
 accatcgagcccaacacttccctggtgttaccacacctggaggagctgaacctgagctacaacggcatcagcact
 gtgctgccctgcccagctccctcgtgtccctgatctcgagcgcaccaacatcctgcagctagacccccaccagc
 40 ctacagggcctgcatgcccctgcgttccctatacatggatggcaactgctactacaagaacctctgcccggggcc
 ctggagggtggccccagggcgcctccttgccctgggcaacctcaccacctgtcactcaagtacaacaacctcaca
 acggtgccccgcagcctgccccctagcctggagtacctgtgttgcctacaaccacattgtcaccttggaacct
 gaggacctggccaatctgactgcccctgcgtgtgctcgatgtgggtggaaactgcccgcgctgtgacctgcacgc
 aacctgcgctggagtgcacacataaatccccagctgcactccgacaccttcagccacctaaagccgctagaa
 45 ggctcgtgttgaaggatagttctctctaccagctgaaccccagatggttccgtggcctgggcaacctcagatg
 ctcgacctgagtgagaacttccctctacgactgctaccaaaccaggcattccagggcctggcccagctgcga
 agactcaactgtccttcaattaccataagaaggtgtccttcgcccactgacgctggcaccctccttcggggagc
 ctgctctccctgcaggaactggacatgcatggcatcttcttcgctcactcagccagaagacgctccagccactg
 gccgcctgcccctgctccagcgtctgtatctgcagatgaacttcatcaaccaggcccagctcggcatcttcaag
 50 gacttccctggctctgcgtacatagacctgtcagacaaccgcatcagtgaggctgtggagccggtggccaccaca
 ggggaggtggatgggtgggaagaaggtctggctgacatccaggacacctcactccaggcccactggacacccccagc
 tctgaggacttcatgccaagctgcaagaacctcagcttccacttgacctgtcacggaacaacctggtaaacagtc
 cagccagagatgtttgcccagctctcgcgcctccagtgctgcgcctgagccacaacagcatctcgaggcggtc

- 16 -

aatggctcacagttcgtgccactgaccagcctgcaggtgctggacctgtccataacaaactggacctgtaccat
 gggcgctcgtttacggagctgccgagctggaggccctggacctcagctacaacagccagcccttcagcatgcgg
 ggtgtggggccacaacctcagctttgtggccagctgccaccctgcgctacctcagcctggcacacaatggcatc
 cacagccgtgtgtcccagcagctctgcagcacctcgctgtgggcccctggacctcagcggcaattccctgagccag
 5 atgtgggctgagggagacctctatctccgcttcttccaaggcctgagaagcctaataccggctagacctgtccag
 aatcgctctgcatacctcctgccatgcaccctgggcaacctccccaagagcttgacgctgctgcgtctccgtaac
 aattacctggccttcttcaattggagcagcctgacctcctgcccacctggaaacctggacctggctggaaac
 cagctgaaggctctgagcaatggcagcctgccttctggcaccagctccagaggctggacctcagcaggaacagc
 atcatcttcgtggtccctggcttcttctgctctggccagaggtgcgagagctcaacctcagtgccaacgcccctc
 10 aggacagaggagccctcctgggttgggttccctagcaggtcccttgaagtcctagatgtgagcgccaacctctg
 cactgcgcctgtggggcagccttctggaccttctgctgcaggttcaggctgcgctggctgctgcccagccctc
 gtcaagtgtggcagtcggggcagctccagggccgagcatcttcgcacaagacctgcgcctctgcctggacaag
 tccctctcctgggactgttttgggtctctcattgctggttgtggccctgggctggccatgcttatgtgcaccac
 ctctgcggtgaggacctctggtactgcttccacctgggctggcctggctgcccggcgggggtggcagcggggc
 15 gcggatgccctgagctatgatgccttctggtgcttcgacaaggcacagagcgagtgccgactgggtgtacaat
 gaactgcgggtgcggctagaggagcgccgtggggcgccggcgctccgctgtgtctggaggagcgtgactggcta
 cctggcaagacgctgttgcgaaacctgtgggctcagctacagcagccgcaagatgctgttctgctggcccac
 acggaccaggtcagtgccctcttgcgtgccagcttctgctggcccagcagcgtctgctggaggacggcagac
 gttgtggtgctggttaactcctgagccctgacgcccgcgttcccggtacgtgcggctgcgcccagcgctctgcgc
 20 cagagtgtcctcttctggccccaccagcctagtggccagcgcagcttctggcccagctaggcatggccctgacc
 agggacaaccgcaacttctataaccagaacttctgcccggggcccgacgatggctgagtagcacagagtgcagcc
 tggcatgtacaacccccagcctgaccttgccctctctgcctatgatgccagctctgcctcactctgtgacgccc
 tgctctgcctccgccacctcaccctggcatacagcaggcactcaataatgccactggcagggccaaacagcca
 aaaaaaaaaaaaaaaaaa

25

SEQ ID NO:16 (Equine TLR9)

atgggccccttgccatgggtgcctgcagccctgtctctcctgggtgcaggcgcccatgctggccgtggctctggcc
 caaggcacctgcctcccttctgcccctgtgagctccagccccacggcctgggtgaactgcaactggctgttctg
 aagtccgtgccccacttctcagcagcagcaccgggacaatgtcaccagccttctctgctctccaaccgcatc
 30 caccacctccagcactccgactttgcccaactgtccaacctgcagaaactcaacctcaaatggaaactgcccgca
 gccggcctcagccccatgcacttcccttgccacatgaccatcgagcccaacacttctctggctgtaccaccctg
 gaggagctgaacctgagctacaacggcatcacgactgtgcctgcctgcccagctccctcgtgtccctgatcctg
 agccgcaccaacatcctgcagctagacccaccagcctcagggcctgcagccctgcgcttccctatacatggat
 ggcaactgctactacaagaacctcggggcgggccctggagggtggccccaggcgccctccttggcctgggcaac
 35 ctacccccactgtcactcaagtacaacaacctcacaacgggtgccccgcagcctgccccctagcctggagtacctg
 ctgttgcctacaaccacattgtcaccttggcaccctgaggacctggccaatctgactgcccctgcgtgtgctcgat
 gtgggtggaaactgccgcgctgtgacctgcaacgcaacctcgcgtggagtggccacataaattccccagctg
 cactccgacaccttcagccacctaaagccgcttagaaggcctcgtgtgaaggatagtctctctaccagctgaac
 cccagatgggttccgtggcctggggcaacctcacagctgcgaagactcaacttgctcctcaattaccataagaagggtgctc
 40 aaaccaaggcattccaggcctggcccagctgcgaagactcaacttgctcctcaattaccataagaagggtgctc
 ttccgctcactcagccagaagacgctccagccactggcccgcctgcccctgctccagcgtctgtatctgcagatg
 aacttcatcaaccaggccagctcggcatcttcaaggacttccctgggtctgcgctacatagacctgtcagacaac
 cgcatcagtgaggctgtggagccggtggccaccacaggggagggtggatgggtgggaaggctcgtgctgacatcc
 45 agggacctcactccaggccactggacacccccagctctgaggacttcatgccaaagctgcaagaacctcagcttc
 accttggacctgtcacggaacaacctggtaacagtcagccagcagagatgtttgcccagctctcgccctccagtg
 ctgcgctgagccacaacagcatctcgaggcggtcaatggctcacagttcgtgccactgaccagcctgcaggtg
 ctggacctgtcccataacaaactggacctgtacctatgggctcgtttacggagctgccgagctggaggccctg
 gacctcagctacaacagccagcccttcagcatgccccgtgtggggccacaacctcagcttctgtggcccagctgccc
 50 accctgcgctacctcagcctggcacacaatggcatccacagccgtgtgtcccagcagctctgcagcaccctcgctg
 tgggcccctggacttcagcggaattccctgagccagatgtgggctgagggagacctctatctccgcttcttccaa
 ggcttgagaagcctaataccggctagacctgtcccagaatcgtctgcataacctcctgccatgcacctgggcaac
 ctccccaaagacttgacgtgctgcgtctccgtaacaattacctggccttcttcaattggagcagcctgaccttc
 ctgcccacacctggaaacctggacctggctggaaacctgagagctgaaggctctgagcaatggcagcctgccttggc
 55 acccagctccagaggctggacgtcagcaggaacagcatcatctcgtggtccctggcttcttctgctctggccag
 aggtgcgagagctcaacctcagtgccaacgcctcaggacagaggagccctcctgggttgggttccctagcaggc
 tcccttgaagtcctagatgtgagcgccaacctctgcactgcgctgtggggcagccttctgtgaccttctgctg

5 MGPYCAPHPLSLLVQAAALAAALAQGTLPAPFLPCELQPRGKVCNWLFLKSVPRFSAGAPRANVTLSLSLISNRIH
HLHSDSFVHLNLRVLNLKWNCPPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSSLVLSLS
RTSILVLGPHTFTGLHALRFLYMDGNCYKNPCQQAWEVAPGALLGLGNLTHLSLKYNNLTEVPRRLPPSLDTLL
LSYNHIITLAPEDLANLTALRVLVDGNCRCRCDHARNPCRECPKNFPKLHPDFTFHLRLEGLVLKDSLSLYKLEK
DWRGLGRRLQVLDLSENFLDYITKTITFRNLTLQRLRLNLSFNYHKVSFAHLQLAPSFGGLVLSLEKLDMHGIFR
10 RLSTNTTLRLPLTQLPKLQSLSLQLNFINQAELSIGAFPSLLFVLDSDNRISGAARPAALGEVDSGVEVWRWRP
GLAPGPLAAVSAKDFMPCSNLNFITDLNLRNLTITIQEQMFTRLRLQLCLRLSHNSISQAVNGSQFVPLTRLRLVLD
LSYNKLDLYHGRSFTELPQLEALDLSYNSQPFMSQGVGHNLFSVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLNLPKSLRQLRLRDNNAFFNWSSSLTVLP
QLEALDLAQNQLKALSNGSLPPGTRLQKLDVSSNSIGFVTPGFFVLNRLKELNLSANALKTVDPPFWFGRLTETL
15 NILDVSPANPLHCACGAADFVLFLEMQAAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETSLDCFGFSLLMVA
LGLAVPMLHLHLCGDLWLYCFHLCLAHLPRLRRRRQGEDTLLYDAFVFDKAQSAVADWVYNELRVQLEERRGRRL
RLCLEERDWLPGKTLFENLWASVYSRKTMTFVLDTRDTRVSGLLRVASFLLAQORLLEDKDVVVLVILRPAAYRSR
YVRLRQRLCRQSVLLWPHQPSGQGSFWANLGMALTRDNRHFYNRNFCRGPTTAE

25 MGPYCAPHPLSLLLVQAAALAAALAQGTLPAPFLPCEIQRGKVCNWLFLKSVPRFSAGAPRANVTSLSLISNRH
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTEIPNTFLAVPTLEELNLSYNGITTVPALPSSSLVLSLS
RTSILVLGPHTFTGLHALRFLYMDGNCYKNPCQQAVEVAPGALLGLGNLTHLSLKYNNLTEVPRRLPPSLDTLL
LSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSISLYKLEK
30 DWFRGLGRQLQVLDLSENFLDYITKTTIFRNLTQLRRNLNLSFNYHKKVSFAHLQLAPSFGGLVSLEKLDMHGIF
RSLTNTTLRPLTQLPKLQSLSLQLNFINQAEISIFGAPPSLLFVDLSDNRISGAARPVAALGEVDSGVEVWRWR
GLAPGPLAAVSAKDFMPSCNLFNFTLDSLNRNVLTIQEQEMFTRLSRQLCLRLSHNSISQAVNGSQFVPLTRLRVLD
LSYNKLDLYHGRSTEDLPQLLEALDLSYNSQPFMSQGVGHNLSSFVAQLPSRLYSLAHNGIHSRVSQKLSSASIRA
LDFSGNSLSQMWAEGLDYLCFFKGLRNLVQLDLSKNHLHTLLPRHLDNLPKSLRQLRLDRNNLAFNNWSSSLTVLP
30 QLEALDLAGNQLKALSNGSLPPGTRLQKLDVSSNSIGFVTPGFFVLANRLKELNLSANALKTVDPFWFGRLTETL
NILDVSANPLHCACGAADFVDFLLEMQAAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETLSDLCFG

gtcggcacgggaagtgagcgccaagcatcetttoetgcagctgccgccaacttgcgcgcagaccctctggaga
35 agccgcatttcctgccatggggccctactgtgccccgacccccctttctctctgggtgcaggcggcggtggc
agcagccctggcccagggcacccctgcttgccttctgccccgtgagctccagccccggggtaagggtgaaatgcaa
ctggctgttcctgaagtctgtgccccgcttttcggccgggagccccccggggccaatgtcaccagcctctccttaat
ctccaaccgcatccaccacttgcacgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagt
40 gaactgccgcgcggcgccctcagccccatgcacttccctgccgcagaccatcgagccccaacaccttctggc
tgtgccaccctggaggagctgaacctgagctacaatggcatcacgacctgcctgccccgccagttctctcgt
atccctgtcgtgagcgcgaccagcatcctggctgtaggccccaccactcaccggcctgcagcgcctcgcctt
tctgtacatggacggcaactctactataagaacccccgccagcaggcgtggaggtggccccaggcgccctcct
tggcctgggcaacctcacgcaacctgtcgtcaagtacaacaacctcacggaggtgccccgcgcctgccccccag
cctggacacctgtctgtctcctacaaccacatcatcacctggcaccgcaggacctggccaatctgactgcct
45 gcgtgtgcttgatgtgggcgggaactgccgcgctgcgaccacgcccgaacccctgcagggagtgccaaagaa
cttccccaaagctgcaccctgacaccttcagccacctgagccgcctcgaaggcctgggtgtgaaggacagtctct
ctacaaactagagaaagactgggttcgcggcctgggcaggctccaagtgtcgacctgagtgagaacttctctta
tgactacatcaccaagaccacatcttcaggaacctgaccagctgcgcgactcaacctgtccttcaattacca
caagaagggtgtccttcgcccaactggcaccctcctttggggggcctgggtgtccttggaagctggacat
50 gcaaggcatcttcttcgctcctccaccaacaccagctccggcgctgaccagctgcccaagctccagagtct
gagctgcagctgaacttcatcaaccaggcgagctcagcatcttctggggccttccccgagcctgctctctgtgga
cctgtcggacaaccgcatcagcggagctgcgagcggtggcgcccttcggggaggtggacagcggggtggaagt
ctggcggtggccaggggcctcgtccaggccgctggcgccgctcagcgcgaaggacttcagccaagctgcaa

- 18 -

cctcaacttcaccttggacctgtcacggaacaacctgggtgacgatccagcaggagatgtttaccgcctctcccg
 cctccagtgccctgcgccctgagccacaacagcatctcgcaggcgggtaatggctcgcagttcgtgcccgtgacccg
 cctgcgagtgctcgacctgtcctacaacaagctggacctgtaccatgggcgctcgttcacggagctgcccagct
 ggaggcactggacctcagctacaacagccagcccttcagcatgcaggcggtgggccacaacctcagcttcgtggc
 5 ccagctgcccgtccctgcgctacctcagccttgcgcacaacggcatccacagccgctgtcacagaagctcagcag
 cgctcgtgcgccctggacttcagcggcaactccctgagccagatgtgggcccaggagacctctatctctg
 ctcttcaaaggcttgaggaaacctgggtccagctggacctgtccaagaaccacctgcacacctcctgctcgtca
 cctggataacctgcccaagagcctgcccagctgctgtcctccgggacaataacctggccttcttcaactggagcag
 cctgactgttctgccccagctggaagccctggatctggcgggaaaccagctgaaggccctgagcaacggcagcct
 10 gccacctggcaccggctccagaagctggacgtgagcagcaacagcatcggttttgtgaccttggttctttgt
 ccttgccaaccggctgaaagagcttaacctcagcgccaacgcctgaagacagtggtaccttctggttcggtcg
 cttaacagagacctgaatatcctagacgtgagcgccaacccgctccactgtgctgccccggcgcccttctgga
 ctctcgtggtgagatgcaggcgccgtgctgggtgtccaggcgctcagctgtggcagtcggggccagctcca
 gggccgcagcatcttcgcacaggacctgcccctctgctggatgagacctctccttggaactgtttggcttctc
 15 gctgctaattggtggcgctggcgctggcgctgcccctgctgcaccacctctgtggctgggacctgtggtactgctt
 ccacctgtgtctggccatttggcccgacggcgccgagcgggcgaggacacctgctctacgatgccttcgt
 ggtcttcgacaaggcgagagtgagtggtggtgtacaacagctccgctgagctggaggagcgccg
 cgggcgccggcgctccgctctgctggaggagcgagactggctccctggcaagacgctcttcgagaacctgtg
 ggctcggctctacagcagccgtaagacctgttctgctggtgaccacacggaccgggtcagtgccctcctgcgcg
 20 cagcttctgctggcccagcagcgctgttgaggagccgaaggatgtcgtggtgctggtgatcctgcccccg
 cgctaccggctccgctacgtgcggtgcccagcgctctgcccagagcgctcctcctctggccccaccagcc
 cagtgggcagggtagcttctgggccaacctgggcatggcctgaccaggagacaaccgaccttctataaccggaa
 ctctgcgggggccccacgacagccgaatagcacagagtgtgcccag

25 SEQ ID NO:20 (Ovine TLR9)

atggggccctactgtgccccgcaccccttctctcctgggtgcaggcgccggcgctggcagcagccctggcccag
 ggcacctgctgcttctgcccctgtgagctccagccccgggtaagggtgaactgcaactggctgttctgaag
 tctgtgcccgcgttttcggccggagcccccgggccaatgtcaccagcctctccttaatctccaaccgcattccac
 30 cacttgacgactctgacttctgtccacctgtccaacctgcgggtcctcaacctcaagtggaaactgcccgcggcc
 ggctcagccccatgcaactccccctgcccagatgacctcgagcccaacaccttctggtgtgcccacctggag
 gagtgaaactgagctacaatggcatcacgacctgctgcccctgcccagttctctcgtatccccgtgctgagc
 cgaccagcatcctgggtgctaggccccaccacttcacggcctgcacgcctgccccttctgtacatggacggc
 aactgctactataagaacctctgccagcaggcgtggaggtggccccagggcgccctccttggcctgggcaacctc
 acgcacctgtcgtcaagtacaacaacctcacggaggtgccccgcgcctgccccccagcctggacacctgctg
 35 ctgctctacaaccacatcatcaccctggcaccgaggacctggccaatctgactgcccctgctgtgtgctgatgtg
 ggcggaactgcccgcgctgcgaccacgcccgaacctgagggagtgcccaaagaacttccccaaagtgcac
 cctgacaccttcagccacctgagccgctcgaaggcctgggtgtgaaggacagttctctctacaaactagagaaa
 gactggttcgcggcctgggcaggctccaagtgtcgacctgagtgagaacttctctatgactacatcaccaag
 accaccatcttcaggaaacctgaccagctgcccagactcaacctgtccttcaattaccacaagaagggtccttc
 40 gccacctgcaactggcaccctccttgggggctggtgtccctggagaagctggacatgcaacggcatcttcttc
 cgctccctcaccaacaccacgctccggccgctgaccagctgcccagctccagagtctgagctgagctgaac
 ttcatacaaccaggccgagctcagcatcttggggccttcccagcctgctctcgtggacctgtcggaacccgc
 atcagcggagctgcgaggccgggtggccgcoctcggggaggtggacagcggggtggaagtctggcggtggccagg
 ggctcgtccaggcccgctggccgctcagcgcaaggacttcacgcaagctgcaacctcaactcaacttg
 45 gacctgtcacggaacaacctgggtgacgatccagcaggagatgtttaccgcctctcccgcctccagtgctgcgc
 ctgagccacaacagcatctcgcaggcgggtaatggctcgcagttcgtgcccgtgaccgcctgagtgctcgac
 ctgtcctacaacaagctggacctgtacctggggcgtcgttcacggagctgccgcagctggaggcactggacctc
 agctacaacagccagccctcagcatgcaggcggtgggccaacacctcagcttctggtggccagctgcccctg
 cgctacctcagccttgcgcacaacggcatccacagccgctgtcacagaagctcagcagcgccctgctgcgcg
 50 ctggacttcagcggcaactccctgagccagatgtgggcccaggagacctctatctctgcttcttcaaaggcttg
 aggaacctggtccagctggacctgtccaagaacctgcacacctcctgctcgtcactggataacctgccc
 aagagcctgcccagctgcttctccgggacaataacctggccttcttcaactggagcagcctgactgttctgccc
 cagctggaagccctggatctggcggaaccagctgaaggccctgagcaacggcagcctgcccactggcaccgg
 ctccagaagctgagcagcaacagcatcggttctgtgacctggcttcttctgcttcttcaaccggctg
 55 aaagagcttaacctcagcgccaacgcctgaagacagtggtaccttctggttcggtcgttcaacagagacctg
 aatatcctagacgtgagcgccaacccgctccactgtgctgccccggcgcccttctggtgacttctgctggagatg

- 19 -

caggcgccgctgacctgggctgtccaggcgctcacgtgtggcagtcggggccagctccagggccgcagcatcttc
gcacaggacctgcgctctgctggatgagaccctctccttggaactgctttggc

Complete nucleotide and amino acid sequences for canine and feline TLR9 are
5 publicly available. For example, an amino acid sequence for canine TLR9 is available as
GenBank accession number BAC65192 and its corresponding nucleotide sequence is
available as GenBank accession number AB104899. An amino acid sequence for feline
TLR9 is available as GenBank accession number AAN15751 and its corresponding
nucleotide sequence is available as GenBank accession number AY137581.

10 Complete nucleotide and amino acid sequences for canine and feline TLR9 were also
determined independently from those available from public databases.

An amino acid sequence of canine TLR9 is provided as SEQ ID NO:21. Based on
comparison with known amino acid sequences of human and murine TLR9, it appears that
SEQ ID NO:21 includes sequence for at least a majority of the extracellular domain, all of the
15 transmembrane domain, and at least a portion of the intracellular domain of canine TLR9
(See Figure 1). Amino acids numbered 1-822 of SEQ ID NO:21 are presumptively
extracellular domain and correspond to SEQ ID NO:22. SEQ ID NO:23 is a nucleotide
sequence of canine TLR9 cDNA having an open reading frame corresponding to nucleotides
91-3186. SEQ ID NO:24 is a nucleotide sequence of canine cDNA encoding amino acids 1-
20 822 of SEQ ID NO:21.

An amino acid sequence of feline TLR9 is provided as SEQ ID NO:25. Based on
comparison with known amino acid sequences of human and murine TLR9, it appears that
SEQ ID NO:25 includes sequence for at least a majority of the extracellular domain, all of the
transmembrane domain, and at least a portion of the intracellular domain of feline TLR9 (See
25 Figure 1). Amino acids numbered 1-820 of SEQ ID NO:25 are presumptively extracellular
domain and correspond to SEQ ID NO:26. SEQ ID NO:27 is a nucleotide sequence of feline
TLR9 cDNA having an open reading frame corresponding to nucleotides 87-3179. SEQ ID
NO:28 is a nucleotide sequence of feline cDNA encoding amino acids 1-820 of SEQ ID
NO:25.

30

SEQ ID NO:21 (Canine TLR9)

MGPCRGALHPLSLVQAAALALALAQGTLPFLPCELQPHGLVNCNWLFLKSVPFRSAAAPRGNTSLSLYSNRI
HHLHDYDFVHFVHLRRLNLKWNCPASLSPMHFPCHMTIEPNTFLAVPTLEDNLNSYNSITTVPALPSSLVLSL
SRTNILLVDPATLAGLYALRFLFLDGNCYKNPCQALQVAPGALLGLGNLTHLSLKYNNTLVVPRGLPPSLEYL

- 20 -

LLSYNHIITLAPEDLANLTALRVLDVGGNCRCDHARNPCRECPKGFPLHPNTFGHLSHLEGLVLRDSSLYSLD
PRWFHGLGNLMVLDLSENFLYDCITKTKAFYGLARLRRLNLSFNYHKKVSFAHLHLASSFGSLLSLQELDIHGIF
FRSLSKTTQLSLAHLPMQLRLHLQLNFISQAQLSIFGAFPLGRYVDLSDNRISGAAPAAATGEVEADCGERVWP
QSRDLALGPLGTPGSEAFMPSCRTLNFTLDLSRNNLVTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL
5 RVLDLSHNKLDLYHGRSFTLPRLEALDLSYNSQPFMSMRGVGHNLFSVAQLPALRYLSLAHNGIHSRVSQQLRSA
SLRALDFSGNTLSQMWAEGDLYLRFFQGLRSLVQLDLSQNRHLHTLLPRNLDNLPKSLRLLRLRDNLYLAFFNWSSL
ALLPKLEALDLAGNQLKALSNGSLPNGTQLQRLDLSGNSIGFVVPSPFFALAVRLRELNLNLSANALKTVEPSWFGSL
AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPLPSRVKCGSPQLQGRSIFAQDLRLCLDEALSWVCFSLSL
10 LAVALSLAVPMLHQLCGWDLWYCFHLCLAWLPRRGRRRRGVDALAYDAFVVFDAQSSVADWVYNELRVQLEERRG
RRALRLCLEERDWPVKTLFENLWASVYSSRKTFLVLRARTDRVSGLLRASFLLAQQRLLEDKDVVVLVILCPDA
HRSRYVRLRQRLCRQSVLLWPHQPSGQRSFQAQLGTALTRDNHRHFNQNFRCGPPTA

SEQ ID NO:22 (Canine TLR9)

MGPCRGALHPLSLVQAAALALALAQGTLPALFLPCELQPHGLVNCNWLFLKSVPRFSAAAPRGNTLSLSLYSNRI
15 HHLHDYDFVHFVHLRRLNLKWNCPASLSPMHFPCHMTIEPNTFLAVPTLEDLNLNSYNSITTVPALPSSIVLSLSL
SRTNIVLDPATLAGLYALRFLFDGNCYYKNPCQQALQVAPGALLGLGNLTHLSLKYNNTTVPRGLPPSLEYL
LLSYNHIITLAPEDLANLTALRVLDVGGNCRCDHARNPCRECPKGFPLHPNTFGHLSHLEGLVLRDSSLYSLD
PRWFHGLGNLMVLDLSENFLYDCITKTKAFYGLARLRRLNLSFNYHKKVSFAHLHLASSFGSLLSLQELDIHGIF
FRSLSKTTQLSLAHLPMQLRLHLQLNFISQAQLSIFGAFPLGRYVDLSDNRISGAAPAAATGEVEADCGERVWP
20 QSRDLALGPLGTPGSEAFMPSCRTLNFTLDLSRNNLVTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL
RVLDLSHNKLDLYHGRSFTLPRLEALDLSYNSQPFMSMRGVGHNLFSVAQLPALRYLSLAHNGIHSRVSQQLRSA
SLRALDFSGNTLSQMWAEGDLYLRFFQGLRSLVQLDLSQNRHLHTLLPRNLDNLPKSLRLLRLRDNLYLAFFNWSSL
ALLPKLEALDLAGNQLKALSNGSLPNGTQLQRLDLSGNSIGFVVPSPFFALAVRLRELNLNLSANALKTVEPSWFGSL
AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPLPSRVKCGSPQLQGRSIFAQDLRLCLDEALSWVCFCS
25

SEQ ID NO:23 (Canine TLR9)

aggaaggggctgtgagctccaagcatcctttcctgagctgctgcccagcctgccagccagaccctctggagaag
ccccgcctccctgtcatgggcccctgcccgtggcgccctgcaccccctgtctctcctggtgaggctgcgcgcta
gcccgtggccctggcccagggcaccctgcccgtcccttccctgcccctgtgagctccagcccatggcctggtgaactgc
30 aactggctgttccctcaagtcctgcccgccttctcgccagctgcaccccgcggtaacgtcaccagcctttccttg
tactccaaccgcatccaccacctccatgactatgactttgtccacttcgtccactgcggcgtctcaatctcaag
tggaaactgcccgcggccagcctcagcccatgacactttccctgtcacatgaccattgagcccaacaccttccctg
gctgtgcccaccctagaggacctgaatctgagctataacagcatcacgactgtgcccgcctgccagttcgctt
gtgtccctgtccctgagccgcaccaacatcctggtgtgtagccctgccaccctggcaggcctttatgccctgcgc
35 ttccctgttccctggaatggcaactgtactacaagaaccctgccagcaggccctgcaggtggccccaggtgccttc
ctggcgctgggcaacctcacacactgtcactcaagtaacaacacctcaccgtggtgcgcggggcctgccccc
agcctggagtaactgtcttctcacaaccacatcatcaccctggcaccctgaggacctggccaatctgactgcc
ctgctgtctcctgatgtgggtgggaactgtgcgcgctgtgacctgcccgtaacccctgcagggagtgcccaag
ggcttccccagctgcacccaacaccttcggccacctgagccacctcgaaggcctggtgttgaggagacgtctt
40 ctctacagcctggaccccaggtggttccatggcctgggcaacctcatggtgtgacctgagtgagaacttccctg
tatgactgcatcaccaaaacaaagccttctacggcctggcccggctgcgcagactcaacctgtccttcaattat
cataagaaggtgtcctttgccacctgcatctggcactcctccttcgggagcctactgtccctgcaggagctggac
atacatggcatcttcttcgctcgctcagcaagaccagcctccagtcgctggcccacctgcccagctccagcgt
ctgcatctgcagttgaactttatcagccaggcccagctcagcatcttcggcgcccttccctggactgcggtacgtg
45 gacttgtcagacaaccgcatcagtgaggctgcagagcccgcggctgccacaggggaggtagaggcagactgtggg
gagagagctctggccacagtcggggaccttgcctctgggcccactgggcaccccggctcagaggccttcatgccc
agctgcaggaccctcaacttcaccttgagcctgtctcggaacaacctagtactgttcagccggagatgtttgtc
cggctggcgcgccctccagtgccctgggctgagccacaacagcatctcgaggcggtcaatggctcgcagttcgtg
cctctgagcaacctgcgggtgctggacctgtccataaacaagctggacctgtaccacgggcgctcgttcacggag
50 ctgcccgggctggaggccttgacctcagctacaacagcagcccttcagcatgcggggcgtggggccacaactctc
agcttctggcacagctgccagccctgcgctacactcagcctggcgccacaatggcatccacagcgcggtgtcccag
cagctccgcagcgcctcgctccggggcctggacttcagtggaataacctgagccagatgtgggcccaggaggagac
ctctatctccgcttcttccaaggcctgagaagcctggttcagctggacctgtcccagaatcgctgcataccctc
ctgccacgcaacctggacaacctcccaagagcctgcggctcctgcggctccgtgacaattacctggcttctctc
55 aactggagcagcctggccctcctaccaagctggaagcctggacctggcgggaaaccagctgaaggcctgagc

- 21 -

aatggcagcttggcccaacggcaccagctccagaggctggacctcagcggcaacagcatcggttcgtgggtcccc
agcttttttgcctggccgtgaggtctcgagagctcaacctcagcgccaacgccctcaagacgggtggagccctcc
tggtttgggtccctggcgggtgccctgaaagtcctagacgtgaccgccaaccccttgcatgtgcgttgcgcgca
accttcgtggacttcttgcctggaggtgcaggtgcggtgcccggcctgcctagccgtgtcaagtgcggcagcccg
5 ggccagctccagggccgcagcatcttcgcacaggacctgcgcctctgcctggacgaagcgctctcctgggtctgt
ttcagcctctcgctgctggctgtggccctgagcctggctgtgcccattgctgcaccagctctgtggctgggacctc
tggtactgcttccacctgtgcctggcctggctgccccggcgggggcgggcggggtgtggatgccctggcctat
gacgccttcgtgggtcttcgacaaggcgagagctcggtggcggaactgggtgtacaatgagctgcgggtacagcta
gaggagcgctggggcgccggcgctacgcctgtgtctggaggaaactgactgggtaccgggcaaaacctcttc
10 gagaacctctgggcctcagtttacagcagccgaagacgtgtttgtgctggcccgacggacagagtgcgcggc
ctcctgcgtgccagcttctgctggcccaacagcgctgctggaggaccgcaaggacgtcgtgggtgctgggtgatc
ctgtgccccgacgcccaccgctcccgtatgtgcggtgcgccagcgccctctgcgccagagtgtcctcctctgg
ccccaccagccagtgccagcgagcttctgggcccagctgggcaaggccctgaccagggacaaccggccacttc
tacaaccagaactctgcccggggcccaagcagcctgtataggcagacagccagcacttcgcgcccctacacc
15 ctgcctgtctgtctgggatgcccagacctgctggctctacaccgcccgtctgtctccctacaccagccctggca
taaagcgaccgctcaataaatgctgctggtagac

SEQ ID NO:24 (Canine TLR9)

atggggccctgcctggcgccctgcacccctgtctctcctgggtgcaggctgcgcgctagccctggccctggcc
20 cagggcacctgcctgccttccctgcctgtgagctccagcccatggcctgggtgaactgcaactggctgttctc
aagtccgtgccccgcttctcggcagctgcaccccgcgtaacgtcaccagccttctcctgtactccaaccgcac
caccacctccatgactatgactttgtccacttcgtccacctgcggcgtctcaatctcaagtggaaactgcccggcc
ggcagctcagccccatgcactttccctgtcacatgaccattgagcccaacaccttccctggctgtgcccacccta
25 gaggacgtgaatctgagctataaacagcatcacgactgtgcccgcctgcccagttcgctgtgtccctgtccctg
agccgcaccaacatcctgggtgctggaccctgccacctggcaggcctttatgccctgcgcttccctgttccctg
ggcaactgctactacaagaacccctgccagcaggccctgcagggtggccccagggtgccctcctgggcctgggcaac
ctcacacacctgtcactcaagtacaacaacctcaccgtgggtgcgcggggcctgccccccagcctggagtacctg
ctcttgccttacaaccacatcatcaccctggcacctgaggacctggccaatctgactgccctgcgtgtcctcgat
gtgggtgggaactgtgcgcgctgtgacccatgcccgttaacccctgcagggagtgcccaagggttccccagctg
30 cccccaacaccttcggccacctgagccacctcgaaggcctgggtgttgaggagacgtctctctacagcctggac
cccagctggaatctgagcctgggcaacctatgggtgctggacctgagtgagaacttccgtgtatgacatgcac
aaaaccaaaagccttctacggcctggcccggtgcgcagactcaacctgtccttcaattatcaagaaggtgtcc
tttggccacctgcacttggcatcctccttcgggagcctactgtccctgcaggagctggacatacatggcatcttc
ttccgctcgctcagcaagaccagctccagtcgctggccacctgccatgctccagcgtctgcacttgcagttg
35 aactttatcagccaggccagctcagcatcttcggcgcttccctggactgcggtacgtggacttgtcagacaac
cgcatcagtgagctgcagagcccgcggtgccacaggggaggttagaggcagactgtggggagagagtctggcca
cagtcggggaccttgctctggggccactgggcaccccggtcagaggccttcatgccagctgcaggaccctc
aactcaccttggaactgtctcggaacaacctagtgcctgttcagccggagatgtttgtccggctggcgccctc
cagtgccctgggctgagccacaacagcatctgcagggtgcaggtcaatggctcgcagttcgtgccttgagcaacctg
40 cgggtgctggacctgtcccataacaagctggacctgtaccacgggcgctcgttcacggagctgcgcggctggag
gccttggacctcagctacaacagccagcccttcagcatgccccggcggtgggcccacaatctcagcttgtggcaag
ctgccagccctgcgctacctcagcctggcgacacatggcatccacagccgctgtcccagcagctccgcagcgcc
tcgctccgggcccctggacttcagtggaataacctgagccagatgtggggccgaggagacctctatctccgcttc
ttccaaggcctgagaagcctgggtcagctggacctgtcccagaatcgccctgcataacctcctgccacgcaacctg
45 gacaacctccccagagcctgcggctcctgcggctccgtgacaattacctggctttcttcaactggagcagcctg
gccctcctacccaagctggaagccctggacctggcgggaaaccagctgaaggccctgagcaatggcagcttgccc
aacggcacccagctccagaggctggacctcagcggaacagcagcagccttcgtgggtccccagctttttgcctg
gcccgtgaggcttcgagagctcaacctcagcgccaacgcctcagacgggtggagccctcctgggttgggtccctg
gcccgtgcccctgaaagtcctagacgtgaccgccaaccccttgcatgtgcgttcggcgcaaccttcgtggacttc
50 ttgctggagggtgcaggctgcgggtgcccggcctgctagccgtgtcaagtgcggcagccggggcagctccagggc
cgcagcatcttcgcacaggacctgcgcctctgcctggacgaagcgtctcctgggtctgtttcagc

SEQ ID NO:25 (Feline TLR9)

MGPCHGALHPLSLLVQAAALAVALAQGTLPALFLPCELQRHGLVNCDWLFLKSVPHFSAAPRGNVTSLSLSYNSRI
55 HHLHDSDFVHLSSLRRLNLKWNCPASLSPMHFPCHMTIEPHTFLAVPTLEELNLSYNSITVTPALPSSSLVLSLSL

- 22 -

SRTNIIIVLDPANLAGLSLRLFLDGNCCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYL
 LLSYNHIIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCMECPKGFPHLHPDTFSLNHLEGLVLKDSLSYLN
 PRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNYHKKVSFAHLHLAPSFGSLLSLQQLDMHGIF
 FRSLSETTLRSLVHLPMQLSLHLMNFINQAQLSIFGAFPLGRYVDLSDNRISGAMELAAATGEVDGGERVRLPS
 5 GDALGPPGTPSPSEGFMPGCKTLNFTLDLSRNNLVITIQPEMFARLSRLQCLLSRNSISQAVNGSQFMPLTSLQV
 LDLSHNKLIDLYHGRSFTELPRLEALDLSYNSQPFMSQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSQQLCSASL
 RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNLRLHTLLPRTLNDLPKSLRLRLRLRDNYLAFFNWSSVL
 LPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVASSFFALATRLRELNLNLSANALKTVEPSWFGSLAG
 TLKVLDVTGNPLHCACGAAFVDFLLEVQAAPVGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDGFLSLLT
 10 VALGLAVPMLHHLHCGWDLWYCFHLCLAWLPRRGRRGADALPYDAFVVFDKAQSAVADWVYNELRVRLEERRGR
 ALRLCLEERDWPGLKTLFENLWASVYSSRKMFLVLAHTDRVSGLLRASFLAQQLLEDKDVVVLVILRPDAHR
 SRYVRLRQLRCQSVLLWPHQPSGQRSFWAQLGTALTRDNQHFYNQNFRCRGPPTAE

SEQ ID NO:26 (Feline TLR9)

15 MGPCHGALHPLSLVQAAALAVALAQGTLPAPFLPCELQRHGLVNCDWLFLKSVPHFSAAAPRGNVTSLSLYSNRI
 HHLHDSDFVHLSLRLNLKWNCPASLSPMHFPCHMTIEPHTFLAVPTLEELNLSYNSITTVPALPSSSLVLSL
 SRTNIIIVLDPANLAGLSLRLFLDGNCCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYL
 LLSYNHIIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCMECPKGFPHLHPDTFSLNHLEGLVLKDSLSYLN
 20 PRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNYHKKVSFAHLHLAPSFGSLLSLQQLDMHGIF
 FRSLSETTLRSLVHLPMQLSLHLMNFINQAQLSIFGAFPLGRYVDLSDNRISGAMELAAATGEVDGGERVRLPS
 GDALGPPGTPSPSEGFMPGCKTLNFTLDLSRNNLVITIQPEMFARLSRLQCLLSRNSISQAVNGSQFMPLTSLQV
 LDLSHNKLIDLYHGRSFTELPRLEALDLSYNSQPFMSQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSQQLCSASL
 RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNLRLHTLLPRTLNDLPKSLRLRLRLRDNYLAFFNWSSVL
 LPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVASSFFALATRLRELNLNLSANALKTVEPSWFGSLAG
 25 TLKVLDVTGNPLHCACGAAFVDFLLEVQAAPVGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDGFCG

SEQ ID NO:27 (Feline TLR9)

agggctctgcgagctccaggcattcttctctgccatcgctgccagctctgccatccagaccctctggagaagcccc
 cactccctgtcatgggccccctgccatggcgccctgcacccccctgtctctcctgggtgcaggctgccgcgctggccg
 30 tggccctggccccaggccaccctgcctgccttctgccctgtgagctccagcgccacggcctgggtgaattgcgact
 ggctgttctcctcaagtcctgcctgccccacttctcggcgccagcgccccctggtaacgtcaccagccttccctgtact
 ccaaccgcacccaccacctccagcactccgactttgtccacctgtccagcctgcggcgtctcaacctcaaattgga
 actgcccacccggccagcctcagccccatgcacttcccctgtcacatgaccattgagccccacaccttccctggccg
 tgcccccctggaggagctgaacctgagctacaacagcatcacgacagtagcccgccctgccagttccctcgtgt
 35 cctgtccttgagccgtaccaacatccctgggtgtggaccctgccaacctcgcagggtgcactccctgcgcttct
 tgttctcctggatggcaactgtactacaagaacctgcccgcaggccctgcaggtggccccggcgccctccttg
 gcctgggcaaccttacgcacctgtcactcaagtaacaacacctcactgcgggtgccccggcgccctgccccagcc
 tggagtaacctgtattgtcctacaaccacatcatcaccctggcacctgaggacctggccaacctgaccgccctgc
 gtgtgctcgatgtgggtgggaactgccgtcgctgtgaccacgcccgaacccctgtatggagtggcccaagggt
 40 tcccgacactgcacccctgacacctcagccacctgaaccacctgaaggcctgggtgtgaaggacagctctctct
 acaacctgaacccagatgggtccatgccctgggcaacctcatggtgctggacctgagtgaagaacttccatatg
 actgcatcaccaaaaccacagccttccagggcctggcccagctgcgcagactcaacttgtcttcaattaccaca
 agaagggtgtccttggccacctgcactggcgccctccttcgggagcctgtctccctgcagcagctggacatgc
 atggcatcttctccgctcgctcagcgagaccacgctccggctcgctgggtccacctgcccagctccagagctctgc
 45 acctgcagatgaacttcatcaatcaggcccagctcagcatcttcggggccttccctggcctgcgatacgtggacc
 tgtcagacaaccgcataagtggagccatggagctggcggtgccacgggggaggtggatgggtggggagagagtc
 ggctgccatctggggacctagctctggggccaccgggcaacccctagctccgagggttcatgccaggctgcaaga
 ccctcaacttcaacttggacctgtcacggaacaacctagtgaacaatccagccagagatgtttgccggctctcgc
 gcctccagtgctcctgagccgaacagcatctcgcaggcagtcacacggctcacaatttatgccgctgacca
 50 gcctgcagggtgctggacctgtcccataacaagctggacctgtacctggggcgtcttccacggagctgcccggc
 tggaggccctggacctcagctacaacagccagccctcagcatgcaggcgtgggtgggtcacaacctcagcttctgg
 cacacctgcccggcctcgctatctcagcctggcgacacacgacatccacagcgtgtgtcccagcagctctgca
 gcgcctcgctggggccttggacttccagcggaatgccttgagccggatgtggggcggaggagacctgtatctcc
 acttcttccgaggcctgaggagcctgggtccgggtggatctgtcccagaatcgctgcataacctcttgcacgca
 55 ccctggacaacctccccagagcctgcggctgtcgtcgtcctcgtagacaattatctggcttcttcaactggagca

- 23 -

gcctggctcctcctccccagggctggaagccctggacctggcgggaaaccagctgaaggccctgagcaacggcagct
 tgcctaataatggaaccagctccagaggctggacctcagcagcaacagtatcagcttcgtggcctccagcttttttg
 ctctggccaccaggctgagagctcaacctcagtgccaacgcccctcaagacgggtggagccctcctgggtcggtt
 ctctagcggggcaccctgaaagtccctagatgtgactggcaacccccctgcactgcgcctgtggggcgcccttcgtgg
 5 acttcttgcctggagggtgcaggctgcagtgcccggtgcccaggccacgtcaagtgtggcagtcagggtcagctcc
 agggccgcagcatctttgcgcaggatctgcgcctctgcctggatgaggccctctcctgggactgttttgccctct
 cgctgctgaccgtggccctgggctggccgtgcccattgctgcaccacctctgtggctgggacctctggtaactgct
 tccacctgtgcctggcctggctgcccggcgggggcgccggcgggcgcgatgcccctgcccctacgatgcctttg
 tggctctcgacaaggcacagagcgcggtggcgactgggtgtacaacgagctgcgggtacggctagaggagcgcc
 10 gtggacgcccagcgctccgctgtgcctggaggaaactgactggctaccgggtaaaacgctctttgagaacctgt
 gggcctcagtttacagcagccgcaagatgctgtttgtgctggccacacagacaggggtcagcgccctcttgcgcg
 ccagctttctgctggcccagcagcgctgctggaggaccgcaaggacgttgggtgctgggtgatcctgcgccccg
 acgcccaccgctcccgtatgtgcggctgcgccagcgctctgcgcagagcgctcctcctctggccccaccagc
 ccagtggccagcgagcttctgggcccagctgggacggccctgaccagggaaccagcacttctataaccaga
 15 acttctgcggggccccacgacggcagagtaccgcccagcaccccaagcctcctacaccttgccctgtctgcctg
 ggatgccggg

SEQ ID NO:28 (Feline TLR9)

atgggcccctgccatggcgccctgcacccctgtctctcctgggtgcaggctgcgcgctggcctggccctggcc
 20 cagggcaccctgcctgcctttctgcctgtgagctccagcgccacggcctgggtgaattgcgactggctgttcctc
 aagtccgtgccccacttctcgggcgagcgccccgtggtaacgtcaccagcctttcctgtactccaaccgcac
 caccacctccagactccgactttgtccacctgtccagcctgcggcgtctcaacctcaaatggaactgccaccc
 gccagcctcagccccatgcacttcccctgtcacatgaccattgagccccacaccttccctggcgctgcccaccctg
 gaggagctgaacctgagctacaacagcatcacgacagtaccgcccctgccagttccctcgtgtccctgtccttg
 25 agccgtaccaacatcctgggtgctggacctgcaacctgcgagggtgcactccctgcgctttctgttccctggat
 ggcaactgctactacaagaacccctgcccgcaggccctgaggtggcccgccgcccctccttggcctgggcaac
 cttacgcacctgtcactcaagtacaacaacctcactgcgggtgcccgcggcctgccccccagcctggagtagctg
 ctattgtcctacaaccacatcatcaccctggcacctgaggacctggccaacctgaccgcccctgcgtgtgctcgat
 gtgggtgggaactgccgtgctgtgaccacgcccgaacccctgtatggagtggcccaagggttcccgcacctg
 30 caccctgacaccttcagccacctgaaccacctcgaaggcctgggtgtgaaggacagctctctctacaacctgaac
 ccagatgggtccatgccctgggcaacctcatgggtgctggacctgagtgagaacttccctatatgactgcatcacc
 aaaaccacagccttccagggcctggccagctgcgacagctcaacttgcctttcaattaccacaagaagggtgtcc
 tttgccacctgcatctggcgccctccttcgggagcctgtcctcctgcagcagctggacatgcatggcatcttc
 ttcgctcgtcagcgagaccagctccggctgctgggtccacctgcccctgctccagagtctgcacctgcagatg
 35 aacttcatcaatcaggcccagctcagcatcttcggggccttccctggcctgcgatacgtggacctgtcagacaac
 cgcataagtggagccatggagctggcggtgcccacgggggaggtggatgggtggggagagagtcgggctgccatct
 ggggacctagctctggggccaccgggacccctagctccgagggttccatggcagggtgcaagacctcaacttc
 accttggacctgtcacggaacaacctagtgaacatccagccagagatgtttgcccggctctcgcgcctccagtgc
 ctgctcctgagccgcaacagcatctcgaggcagtcacggctcacaatttatgcccgtgaccagcctgcagggtg
 40 ctggacctgtcccataacaagctggacctgtaccatggcgctctttcaccggagctgcgcggctggaggccctg
 gacctcagctacaacagccagcccttcagcatgcaggcggtgggtcacaacctcagctttgtggcacagctgcgc
 gccctgcgctatctcagcctggcgcaacaacgacatccacagccgtgtgtcccagcagctctgcagcgcctcgtg
 cgggccttggacttcagcggcaatgccttgagccggatgtgggcccaggagacctgtatctccacttcttccga
 ggccctgaggagcctgggtccggttgatctgtcccagaatcgctgcataccctcttggccacgcacctggacaac
 45 ctccccaaagagcctgcggctgctgcgtctccgtgacaattatctggctttcttcaactggagcagcctggctcctc
 ctccccaggctggaagccctggacctggcgggaaaccagctgaaggccctgagcaacggcagcttgccaatgga
 acccagctccagaggctggacctcagcagcaacagtatcagcttcgtggcctccagcttttttgccttggccacc
 aggtgcgagagctcaacctcagtgccaacgcccctcaagcgggtggagccctcctgggtctctctagcgggc
 accctgaaagtccctagatgtgactggcaacccccctgcactgcgcctgtggggcgccctcgtggacttctgctg
 50 gaggtgcaggctgcagtgcccggcctgcccaggccacgtcaagtgtggcagtcagggtcagctccaggggccgcagc
 atctttgcgcaggatctgcgcctctgcctggatgaggccctctcctgggactgttttggc

Complete nucleotide and amino acid sequences for murine and human TLR9 are publicly available. For example, an amino acid sequence of murine TLR9 is available as

- 24 -

GenBank accession no. AAK29625, provided as SEQ ID NO:29. Amino acids numbered 1-821 of SEQ ID NO:29 presumptively include the entire extracellular domain and correspond to SEQ ID NO:30. SEQ ID NO:31 corresponds to GenBank accession number AF348140, which is a nucleotide sequence of murine TLR9 cDNA. SEQ ID NO:32 is a nucleotide sequence of murine cDNA encoding amino acids 1-821 of SEQ ID NO:29.

An amino acid sequence of human TLR9 is available as GenBank accession no. AAF78037, provided as SEQ ID NO:33. Amino acids numbered 1-820 of SEQ ID NO:33 presumptively include the entire extracellular domain and correspond to SEQ ID NO:34. SEQ ID NO:35 corresponds to GenBank accession number AF245704, which is a nucleotide sequence of human TLR9 cDNA. SEQ ID NO:36 is a nucleotide sequence of human cDNA encoding amino acids 1-820 of SEQ ID NO:33.

SEQ ID NO:29 (Murine TLR9)

MVLRRRTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAASCSNITRLSLISNRI
 15 HHLHNSDFVHLSNLRQLNLKWNCPPTGLSPLHFSCHMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNLSSL
 SHTNIVLDANSLAGLYSLRVLFMDGNCYKPNCTGAVKVTPGALLGLSNLTHLSLKYNLTKVPRQLPPSLEYL
 LVSYNLIVKLGPEDLANLTSLRVLDVGGNCRCDHAPNPCIIECGQKSLHLHPETFHHLSHLEGLVLKDSSLHTLN
 SSWFQGLVNLVLDLSENFLYESINHTNAFQNLTRLRLKLNLSFNRYRKKVSFARLHLASSFKNLVSLQELNMNGIF
 20 FRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRFVDLSNDRISGPSTLSEATPEEADDAEQEELL
 SADPHAPLSTPASKNFMDRCKNFKFTMDLSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ
 VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFMSKGIGHNFSFVAHLSMLHSLSLAHNDIHTRVSSHLNSNS
 VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLDLSQNNLHILRPQNLNLPKSLKLLSLRDNYLSFFNWTSL
 FLPNLEVLDLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV
 25 MNLTVLVDVRSNPLHCACGAADFVLDLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFGLSLL
 AVAVGMVVPILHHLCGWDVWYCFHLCLAWLPLLARSRRSAQALPYDAFVVFDDKAQSAVADWVYNELRVRLREERRG
 RRALRLCLEDRDLWPGQTLFENLWASITYGSRKTLFVLAHTDRVSGLLRTSFLLAQQRLLEDKDVVVLVILRPDA
 HRSRYVRLRQRLCRQSVLFWPQQPNGQGGFWAQLSTALTRDNRHFYNQNFRCRGPTAE

SEQ ID NO:30 (Murine TLR9)

MVLRRRTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAASCSNITRLSLISNRI
 30 HHLHNSDFVHLSNLRQLNLKWNCPPTGLSPLHFSCHMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNLSSL
 SHTNIVLDANSLAGLYSLRVLFMDGNCYKPNCTGAVKVTPGALLGLSNLTHLSLKYNLTKVPRQLPPSLEYL
 LVSYNLIVKLGPEDLANLTSLRVLDVGGNCRCDHAPNPCIIECGQKSLHLHPETFHHLSHLEGLVLKDSSLHTLN
 35 SSWFQGLVNLVLDLSENFLYESINHTNAFQNLTRLRLKLNLSFNRYRKKVSFARLHLASSFKNLVSLQELNMNGIF
 FRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRFVDLSNDRISGPSTLSEATPEEADDAEQEELL
 SADPHAPLSTPASKNFMDRCKNFKFTMDLSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ
 VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFMSKGIGHNFSFVAHLSMLHSLSLAHNDIHTRVSSHLNSNS
 VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLDLSQNNLHILRPQNLNLPKSLKLLSLRDNYLSFFNWTSL
 40 FLPNLEVLDLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV
 MNLTVLVDVRSNPLHCACGAADFVLDLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFG

SEQ ID NO:31 (Murine TLR9)

tgtcagagggagcctcgggagaatcctccatctcccaacatggttctccgtcgaaggactctgcaccccttgctcc
 ctcttggtacaggctgcagtgctggctgagactctggcctgggtaccctgcctgcttctaccctgtgagctg

- 25 -

aagcctcatggcctgggtggactgcaattggctgttctgaagtctgtaccccggtttctctgcggcagcatcctgc
 tccaacatcaccgcctctccttgatctccaaccgtatocaccacctgcacaactccgacttcgtccacctgtcc
 aacctgcggcagctgaacctcaagtggaaactgtccacccactggccttagccccctgcacttctcttgccacatg
 accattgagcccagaaccttctcctgggtatgctgacactggaggagctgaacctgagctataatggtatcaccact
 5 gtgccccgactgcccagctccctgggtgaatctgagcctgagccacaccaacatcctgggtctagatgctaacagc
 ctgcccggcctatacagcctgcgcgttctcttcatggaggggaactgctactacaagaacctgcacaggagcg
 gtgaagggtgaccccaggcgccctcctgggctgagcaatctcaccatctgtctctgaagtataacaacctcaca
 aagggtgccccgccaactgccccccagcctggagtacctcctgggtgctctataacctcattgtcaagctggggcct
 gaagacctggccaatctgacctcccttcgagtacttgatgtgggtgggaattgcgctcgctgcgacctgcccc
 10 aatccctgtatagaatgtggccaaaagtcctccacctgcacctgagaccttccatcacctgagccatctggaa
 ggctgggtgctgaaggacagctctctccatacactgaactcttctcctgggtccaaggctgtggtcaacctctcggtg
 ctggacctgaagcaacttctctatgaagcatcaaccacaccaatgccttccagaacctaacccgctgcgc
 aagctcaacctgtccttcaattaccgcaagaaggtatcttggccgctccacctggcaagttccttcaagaac
 ctgggtgctactgcaggagctgaacatgaacggcatcttcttccgctcgctcaacaagtacacgctcagatggctg
 15 gccgatctgcccacactccacactctgcatcttcaaatgaacttcatcaaccaggcacagctcagcatcttgggt
 accttccgagcccttcgcttctgtggacttgctcagacaatcgcatcagtgggccttcaacgctgtcagaagccacc
 cctgaagaggcagatgatgcagagcaggaggagctgtgtctgctggatcctcaccagctccactgagcaccct
 gcttctaagaacttcatggacaggtgtaagaacttcaagttcaccatggacctgtctcggaacaacctgggtgact
 atcaagccagagatgttgtcaatctctcagcctccagtgctttagcctgagccacaactccattgcacaggct
 20 gtcaatggctctcagttcctgcccgtgactaatctgcaggtgctggacctgtccataaacaactggacttgtac
 cactggaaatcgttcaagtgaactacacagttgcaggcctggacctgagctacaacagccagcctttagcatg
 aagggtataggccacaatttcaagtttctgtggccatctgtccatgctacacagccttagcctggcacacaatgac
 attcataaccctgtgtctcctacatctcaacagcaactcagtgaggttcttgaacttcagcggcaacgggtatgggc
 cgcgtgtgggatgaggggggcttctcctcatttcttccaaggcctgagtgccctgctgaagctggacctgtct
 25 caaataacctgcatactcctccggccccagaaccttgacaacctccccaaagagcctgaagctgctgagcctccga
 gacaactacatcttcttctaactggaccagctgtctcctcctgccccacctggaagtcttagacctggcaggc
 aaccagctaaaggcctgaccaatggcaccctgcctaatggcaccctcctccagaaactggatgtcagcagcaac
 agtatcgtctctgtgggtcccagccttcttgccttggcggtgctgagctgaaagaggtcaacctcagccacaact
 ctcaagacgggtggatcgctcctgggttggggccattgtgatgaacctgacagttctagacgtgagaagcaacct
 30 ctgcactgtgctgtggggcagccttcgtagacttactgttggaggtgcagaccaaggtgcctggcctggcta
 ggtgtgaagtgtggcagccccggccagctgcagggccgtagcatcttcgcacaggacctgcggctgtgctggat
 gaggtcctctcttgggactgcttggccttcaactcttggctgtggccgtgggcatggtggtgctataactgcac
 catcttgcggctgggacgtctggtactgttttcatctgtgctggcatggctaccttctgctggcccgagccga
 cgcagcggcaagctctccctatgatgccttctggtgttgcgataaggcacagagcgcaggttgcggactgggtg
 35 tataacgagctgcgggtgcggctggaggagcggcggtgctcgagccctacgcttctgtctggaggaccgagat
 tggctgctggccagacgtcttctcgagaacctctgggcttccatctatgggagccgcaagactctatttggctg
 gccacacggaccgcgtcagtgccctcctgcgcaccagcttctgctggctcagcagcgcctgttgaagaccgc
 aaggacgtggtgtgtgtggtgatcctgcgtccggatgcccaccgctcccgtatgtgcgactgcccagcgtctc
 tgccgccagagtgtgctcttctggccccagcagcccaacgggcaggggggcttctgggccagctgagtacagcc
 40 ctgactagggacaacggccacttctataaccagaacttctgcccgggacctacagcagaatagctcagagcaaca
 gctggaaacagctgcatcttcatgcctggttcccagattgtctgctgctgc

SEQ ID NO:31 (MURINE TLR9)

atggttctccgtcgaaggactctgcaccccttgtccctcctgggtacaggctgcagtgctgggtgagactctggcc
 45 ctgggtaccctgcctgccttccctaccctgtgagctgaagcctcatggcctgggtgactgcaattggctgttccctg
 aagtctgtaccccggttctctgcggcagcactcctgctccaacatcaccgcctctccttgatctccaaccgtatc
 caccacctgcacaactccgacttcgtccacctgtccaacctgcccagctgaacctcaagtggaaactgtccaccc
 actggccttagccccctgcacttctcttgccacatgaccattgagcccagaaccttctcctggctatgcgtacactg
 50 gaggagctgaacctgagctataatggtatcaccactgtgccccgactgccagctccctgggtgaatctgagcctg
 agccacaccaacatcctggttctagatgctaacagcctgcgcggcctatacagcctgcgcgttctcttcatggac
 gggaaactgctactacaagaaccttgcacaggagcgggtgaagggtgaccccaggcgccctcctgggctgagcaat
 ctacccatctgtctctgaagtataacaacctcacaagggtgccccgccaactgccccccagcctggagtacctc
 ctgggtgctctataacctcattgtcaagctggggcctgaagacctggccaatctgacctcctctcagtagtactgat
 55 gtgggtgggaattgcccgtcgctgcgacctgcccccaatccctgtatagaatgtggccaaaagtcctccacttg
 caccctgagaccttccatcacctgagccatctggaaggcctgggtgctgaaggacagctctctccatacactgaac
 tcttctcctgggtccaaggctgtggtcaacctctcggtgctggacctgaagcagaaacttctctatgaagcatcaac
 cacaccaatgccttccagaacctaacccgctgcgcaagctcaacctgtccttcaattaccgcaagaaggtatcc

- 26 -

tttgcccgcctccacctggcaagttccttcaagaacctggtgtcactgcaggagctgaacatgaacggcatcttc
 ttccgctcgctcaacaagtagacgctcagatggctggcgatctgccaaactccacactctgcatcttcaaag
 aacttcatcaaccaggcacagctcagcatctttggtaccttccgagcccttcgctttgtggacttgtcagacaat
 cgcacagtggtggccttcaacgctgtcagaagccacccctgaagaggcagatgatgcagagcaggaggagctgttg
 5 tctgcgatcctcaccagctccactgagcaccctgcttctaagaacttcatggacaggtgtaagaacttcaag
 ttcacatggacctgtctcggaacaacctggtgactatcaagccagagatgtttgtcaatctctcagcctccag
 tgtcttagcctgagccacaactccattgcacaggctgtcaatggctctcagttcctgcccgtgactaatctgcag
 gtgctggacctgtcccataaacaactggacttgcaccactggaaatcggttcagtgagctaccacagttgcaggcc
 ctggacctgagctacaacagccagcccttagcatgaagggtataggccacaatttcagttttgtggcccatctg
 10 tccatgtcacacagccttagcctggcacacaatgacattcatacccggtgtgtcctcacatctcaacagcaactca
 gtgaggtttcttgacttcagcggcaacgggtatgggcccagatgtgggatgagggggcctttatctccatttcttc
 caaggcctgagtggtgctgaagctggacctgtctcaaaataacctgcatatcctccggccccagaaaccttgac
 aacctcccaagagcctgaagctgctgagcctccgagacaactacctatctttctttaactggaccagtctgtcc
 ttcttgcacaacctggaagtcttagacctggcaggcaaccagctaaaggccctgaccaatggcaccctgcctaat
 15 ggcacctctccagaaactggatgtcagcagcaaccagctaatggctctctgtgtgtcccagccttctcgctctggcg
 gtcgagctgaaagaggtcaacctcagccacaacattctcaagacgggtggatcgctcctgggtttgggcccattgtg
 atgaacctgacagttctagacgtgagaagcaacctctgcactgtgctgtggggcagccttcgtagacttactg
 ttggaggtgcagaccaaggtgctggcctggctaagtgtgtaagtgtggcagccccggccagctgcagggccgt
 agcatcttcgcacaggacctgcccgtgtgcctggatgaggtcctctcttgggactgctttggc
 20

SEQ ID NO:33 (Human TLR9)

MGFCRSALHPLSLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRI
 HHLHDSDFAHLPRLRLNLKWNCPVGLSPMHFPCMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSL
 SHTNIMLDSASLAGLHALRFLFMDGNCYKNPCRQALEVAPGALLGLGNLTHLSLKYNNTVVPRLPSSLEYL
 25 LLSYNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNCPMECPRHFPQLHPDTFSHLRLEGLVLKDSLSWLN
 ASWFRGLGNLRVLDLSENFLYKCTTKTKAFQGLTQRLKLNLSFNQKRVSAHLSLAPSGSLVALKELDMHGIF
 FRSLDETTLRPLARLPMQLTLRLQMNFINQAQLGIFRAFPGLRYVDLSNDRISGASELTATMGEADGGEKVLWLP
 GD LAPAPVDTPSSEDFRPNCTLNFTLDLSRNNLVTVPQEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV
 LDLSRNKLDLYHEHSFTLPRLEALDLSYNSQPFQMVGHNFSFVAHLRLTLRHLSLAHNNIHSQVSQQLCSTSL
 30 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNRHLTLPLQTLRLNPKSLQVLRRLDNYLAFFKWWSLHF
 LPKLEVLDLAGNRLKALTNGSLPAGTRLRLRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDSHWFGLAS
 ALQILDVSPANPLHCACGAAFMDFLLEVQAAPVGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLA
 VALGLGVPMLHHLGWDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVDKTSQSAVADWVYNELRGQLEECRG
 RWALRLCLEERDWPGLKTLFENLWASVYGSRTFLVLAHTDRVSGLLRASFLLAQQRLLEDKDVVVLVILSPDG
 35 RRSRYVRLRQLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHNFYNRNFCQGPTAE

SEQ ID NO:34 (Human TLR9)

MGFCRSALHPLSLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRI
 HHLHDSDFAHLPRLRLNLKWNCPVGLSPMHFPCMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSL
 40 SHTNIMLDSASLAGLHALRFLFMDGNCYKNPCRQALEVAPGALLGLGNLTHLSLKYNNTVVPRLPSSLEYL
 LLSYNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNCPMECPRHFPQLHPDTFSHLRLEGLVLKDSLSWLN
 ASWFRGLGNLRVLDLSENFLYKCTTKTKAFQGLTQRLKLNLSFNQKRVSAHLSLAPSGSLVALKELDMHGIF
 FRSLDETTLRPLARLPMQLTLRLQMNFINQAQLGIFRAFPGLRYVDLSNDRISGASELTATMGEADGGEKVLWLP
 GD LAPAPVDTPSSEDFRPNCTLNFTLDLSRNNLVTVPQEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV
 45 LDLSRNKLDLYHEHSFTLPRLEALDLSYNSQPFQMVGHNFSFVAHLRLTLRHLSLAHNNIHSQVSQQLCSTSL
 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNRHLTLPLQTLRLNPKSLQVLRRLDNYLAFFKWWSLHF
 LPKLEVLDLAGNRLKALTNGSLPAGTRLRLRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDSHWFGLAS
 ALQILDVSPANPLHCACGAAFMDFLLEVQAAPVGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFA

50 SEQ ID NO:35 (Human TLR9)

aggctggtataaaaaatcttacttctctattctctgagccgctgctgcccctgtgggaagggaacctcgagtgtga
 agcatccttcctgtagctgctgtccagctctgcccgccagaccctctggagaagccctgccccagcatgggt
 ttctgcccgcagcgcctgcaccgcgtgtctctcctggtgcaggccatcatgctggccatgaccctggccctgggt

- 27 -

accttgctgcttcttaccctgtgagctccagccccagggctggtgaactgcaactggctgttcttgaagtct
gtgccccacttctccatggcagcaccctgtggcaatgtcaccagccttcttctgtcctccaaccgcatccaccac
ctccatgattctgactttgccacctgccagcctgcgccatctcaacctcaagtggaactgcccgcgggtggc
ctcagccccatgcacttcccctgccacatgaccatcgagcccagcaccttcttggctgtgcccacccctggaagag
5 ctaaactgagctacaacaacatcatgactgtgctgcgctgcccacatccctcatatccctgtccctcagccat
accaacatcctgatgctagactctgccagcctcgccggcctgcatgccctgcgcttcttattcatggacggcaac
tgttattacaagaacccttgcaggcaggcactggaggtggccccgggtgccctccttggcctgggcaacctcacc
cacctgtcactcaagtacaacaacctcactgtggtgccccgcaacctgccttccagcctggagtatctgtgttg
tcctacaaccgcatcgtcaaaactggcgctgaggacctggccaatctgaccgcccctgcgtgtgctcgatgtgggc
10 ggaaattgcccgcgctgcgaccacgctcccaaccctgcatggagtgcctcgtcacttccccagctacatccc
gataccttcagccacctgagccgtcttgaaggcctgggtgttgaaggacagttctctctcctggctgaatgccagt
tggttccgtgggctgggaaacctccgagtgctggacctgagtgagaacttctctacaaatgcatcactaaaacc
aaggccttccagggcccatacacagctgcgcaagcttaacctgtccttcaattacaaaagaggggtgccttggcc
cacctgtctctggcccccttcttccgggagcctggctgcctggaaggagctggacatgcacggcatcttcttccgc
15 tcaactgatgagaccacgctccggccactggccgcctgcccctgcatgctccagactctgcgtctgcagatggaacttc
atcaaccaggcccagctcgccatcttccgggccccttccctggcctgcgtacgtggacctgtcggacaaccgcatc
agcggagcttccggagctgacagccaccatgggggaggcagatggaggggagaaggctctggctgcagcctggggac
cttgcctccggccccagtgagcactcccagctctgaagacttccaggcccaactgcagcaccctcaacttccacttg
gatctgtcacggaacaacctgggtgacctgcagccggagatgtttgccagctctcgcacctgcagtgcctgcgc
20 ctgagccacaactgcatctcgaggcagtcattggctcccagttcctgcccgtgacccggtctgcaggtgctagac
ctgtcccgcaataagctggacctctaccacgagcactcattcacggagctaccgcgactggaggccctggacctc
agctacaacagccagcccttggcctgcaggcgtggggccacaacttcagcttctgtggctcacctgcgcacctg
cgccacctcagcctggccccacaacaacatccacagccaagtgtcccagcagctctgcagtagctgcgtgcgggccc
ctggacttccagcggcaatgcactgggcccatagtgggcccagggagacctctatctgcacttcttccaaggcctg
25 agcggtttgatctggctggacttgtcccagaaccgctgcacaccctcctgccccaaacctgcgcaacctcccc
aagagcctacaggtgctgcgtctccgtgacaattacctggccttctttaaagggtggagcctccacttcttgcct
aaactggaagtctcgcactggcaggaaaccggctgaaggccctgaccaatggcagcctgcctgctggcaccocgg
ctccggaggctggatgtcagctgcaacagcatcagcttctgtggcccccggttcttttccaaggccaaggagctg
cgagagctcaaccttagcgccaacgcctcaggcagctggcggcaaacctcctgggttggggccctggcgccctgcgtg
30 caaatactagatgtaagcgccaacctctgcactgcgcctgtggggcgccctttaaaggacttctgctggagggtg
caggctgcctgcccggctgtcccagccgggtgaagtgtggcagtcggggccagctccaggggcctcagcatcttt
gcacaggacctgcgcctctgcctggatgaggccctctcctgggactgttctgcctctcgtgctggctgtggct
ctgggcccgtgggtgtgcccctgctgcacacctctgtggctgggacctctggtactgcttccacctgtgcctggcc
tggttccctggcgggggcgccaaagtggcgagatgaggatgcctgcctacgatgccttctgtggtctctgcac
35 aaaaacgcagagcgcagtgaggactgggtgtacaacgagcttccggggcagctggaggagtgcctggcgctgg
gcactccgcctgtcctggaggaacgcgactgtgctggcggcaaacctcttggagaaaccttggggcctcggctc
tatggcagccgcaagacgctgtttgtgctggccccacagggaccgggtcagtggtctcttgcgcgccagcttctg
ctggcccagcagcgcctgtggaggaccgcaaggacgtcgtgggtgctgggtgatcctgagccctgacggccgcgc
tcccgtacgtgcggctgcgccagcgcctctgcccagagtgctcctccttggccccaccagcccagtggtcag
40 cgagcttctggggccagctgggcatggccctgaccagggacaaccaccacttctataaccggaactctgcccag
ggacccacggccgaatagccgtgagccggaatcctgcacgggtgccacctccacactcacctcacctctgcctgcc
tggtctgacctcccctgctgcctcctcaccacaacctgacacagagca

SEQ ID NO:36 (Human TLR9)

atggggtttctgcccagcgccttgcacccgctgtctctcctgggtgcaggccatcatgctggccatgacctggcc
ctgggtaccttgctgccttccctaccctgtgagctccagccccacggcctggtgaactgcaactggctgttctg
aagtctgtgccccacttctccatggcagcaccctgtggcaatgtcaccagccttcttctgtcctccaaccgcatc
caccacctccatgattctgactttgccacctgccagcctgcgccatctcaacctcaagtggaactgcccgcgcg
gttggcctcagccccatgcacttcccctgccacatgaccatcgagcccagcaccttcttggctgtgcccacccctg
50 gaagagctaaacctgagctacaacaacatcatgactgtgctgctgcccacatccctcatatccctgtccctc
agccataccaacatcctgatgctagactctgccagcctcgccggcctgcatgccctgcgcttcttattcatggac
ggcaactgttattacaagaacccttgcaggcaggcactggaggtggccccgggtgccctccttggcctgggcaac
ctcaccacactcactcaagtacaacaacctcactgtggtgccccgcaacctgccttccagcctggagtagatctg
ctgttgcctacaaccgcatcgtcaaaactggcgctgaggacctggccaatctgaccgcccctgcgtgtgctcgat
55 gtggggcggaattgcccgcgctgcgaccacgctcccaaccctgcatggagtgcctcgtcacttccccagcta
catcccgataccttccagccacctgagccgtcttgaaggcctgggtgttgaaggacagttctctctcctggctgaat
gccagttgggttccgtgggctgggaaacctccgagtgctggacctgagtgagaacttctctacaaatgcatcact

- 28 -

5 aaaaccaaggccttccagggcctaacacagctgcgcaagcttaacctgtccttcaattacaaaaagaggggtgtcc
 tttgcccacctgtctctggcccttccctcgggagcctggcgcctgaaggagctggacatgcacggcatcttc
 tccgctcactcgatgagaccagctccggccactggccgcctgcccatgctccagactctgcgtctgcagatg
 aacttcatcaaccaggcccagctcggcatcttcagggccttccctggcctgcgctacgtggacctgtcggacaac
 10 cgcacagcggagcttcggagctgacagccaccatgggggaggcagatggaggggagaaggtctggctgcagcct
 ggggacctgtctccggccccagtggaactcccagctctgaagacttcaggcccaactgcagcacctcaacttc
 accttggatctgtcacggaacaacctgggtgaccgtgcagccggagatgtttgccagctctcgcacctgcagtgc
 ctgcgctcagccacaactgcatctcgcaggcagtcgaatggctcccagttcctgcccgtgacccgtctgcaggtg
 ctagacctgtcccgaataagctggacctctaccagagcactcattcacggagctaccgcgactggagccctg
 15 gacctcagctacaacagccagccctttggcatgcagggcgtgggcccacaacttcagcttcgtggctcacctgcgc
 acctgcgccacctcagcctggcccaacaacatccacagccaagtgtcccagcagctctgcagtacgtcgctg
 cgggcccctggacttcagcggcaatgcactgggcatatgtgggcccaggagacctctatctgcacttcttccaa
 ggctgagcgggtttgatctggctggactgtcccagaaccgcctgcacaccctcctgccccaaacctgcgcaac
 20 ctccccaagagcctacaggtgctgcgtctccgtgacaattacctggccttctttaagtggtggagcctccacttc
 ctgccccaaactggaagtctcgcacctggcaggaaccggctgaaggccctgaccaatggcagcctgctgtggc
 accggctccggaggtggatgtcagctgcaacagcatcagcttcgtggcccccggttcttttcaaggccaag
 gagctgcgagagctcaaccttagcgccaacgcctcaagacagtggaccactcctgggtttgggccccctggcgagt
 gccctgcaataactagatgtaagcgccaacctctgcactgcgcctgtggggcgccctttatggacttctgtgtg
 gaggtgcaggtgcccgtgcccggctgtcccagccgggtgaagtgtggcagtcggggccagctccaggccctcagc
 atctttgcacaggacctgcgcctctgcctggatgaggccctctcctgggactgtttcgcc

In addition to the foregoing native rat, porcine, bovine, equine, and ovine TLR9
 polypeptides and nucleic acid molecules encoding them, chimeric TLR9 polypeptides and
 nucleic acid molecules encoding them are provided by the invention. The chimeric
 25 polypeptides include at least one amino acid substitution based on a comparison of
 conserved and non-conserved amino acids among at least two of rat, murine, porcine, bovine,
 equine, ovine, canine, feline, and human TLR9. The information contained in a multiple
 sequence alignment of these various TLR9 polypeptide sequences, provided for example in
 Figure 1, can be used to identify and select individual amino acid positions and even
 30 individual amino acids to substitute in designing a chimeric TLR9. The substitution or
 substitutions can be effected using methods known to those of ordinary skill in molecular
 biology. Nucleic acids encoding the native or chimeric polypeptides of the invention can be
 inserted into an expression vector and used to express TLR9 polypeptide.

A conservative amino acid substitution shall refer to a substitution of a first amino
 35 acid for a second amino acid, wherein side chains of the first amino acid and the second
 amino acid share similar features in terms of hydrophobicity, size, aromaticity, or tendency to
 alter conformation. For example, conservative amino acid substitutions generally may be
 made between members within each of the following groups: hydrophobic (A, I, L, M, V),
 neutral (C, S, T), acidic (D, E), basic (H, K, N, Q, R), and aromatic (F, W, Y). A non-
 40 conservative amino acid substitution refers to any other amino acid substitution.

- 29 -

An expression vector for TLR9 will include at least a nucleotide sequence coding for a TLR9, or a fragment thereof coding for a functional TLR9 polypeptide, operably linked to a gene expression sequence which can direct the expression of the TLR9 nucleic acid within a eukaryotic or prokaryotic cell. A "gene expression sequence" is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the nucleic acid to which it is operably linked. With respect to TLR9 nucleic acid, the "gene expression sequence" is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the TLR9 nucleic acid to which it is operably linked. The gene expression sequence may, for example, be a mammalian or viral promoter, such as a constitutive or inducible promoter. Constitutive mammalian promoters include, but are not limited to, the promoters for the following genes: hypoxanthine phosphoribosyl transferase (HPRT), adenosine deaminase, pyruvate kinase, β -actin promoter, and other constitutive promoters. Exemplary viral promoters which function constitutively in eukaryotic cells include, for example, promoters from the simian virus (e.g., SV40), papillomavirus, adenovirus, human immunodeficiency virus (HIV), Rous sarcoma virus (RSV), cytomegalovirus (CMV), the long terminal repeats (LTR) of Moloney murine leukemia virus and other retroviruses, and the thymidine kinase (TK) promoter of herpes simplex virus. Other constitutive promoters are known to those of ordinary skill in the art. The promoters useful as gene expression sequences of the invention also include inducible promoters. Inducible promoters are expressed in the presence of an inducing agent. For example, the metallothionein (MT) promoter is induced to promote transcription and translation in the presence of certain metal ions. Other inducible promoters are known to those of ordinary skill in the art.

In general, the gene expression sequence shall include, as necessary, 5' non-transcribing and 5' non-translating sequences involved with the initiation of transcription and translation, respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribing sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined nucleic acid coding sequence for a TLR9 polypeptide. The gene expression sequences optionally include enhancer sequences or upstream activator sequences as desired.

- 30 -

Generally a nucleic acid coding sequence and a gene expression sequence are said to be “operably linked” when they are covalently linked in such a way as to place the transcription and/or translation of the nucleic acid coding sequence under the influence or control of the gene expression sequence. Thus the TLR9 nucleic acid coding sequence and the gene expression sequence are said to be “operably linked” when they are covalently linked in such a way as to place the transcription and/or translation of the TLR9 nucleic acid coding sequence under the influence or control of the gene expression sequence. If it is desired that the TLR9 sequence be translated into a functional protein, two DNA sequences are said to be operably linked if induction of a promoter in the 5' gene expression sequence results in the transcription of the TLR9 sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the TLR9 sequence, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a gene expression sequence would be operably linked to a TLR9 nucleic acid sequence if the gene expression sequence were capable of effecting transcription of that TLR9 nucleic acid sequence such that the resulting transcript might be translated into the desired TLR9 protein or polypeptide.

A “TLR9 ligand” as used herein refers to a molecule that specifically binds a TLR9 polypeptide. In one embodiment the TLR9 ligand specifically binds a TLR9 polypeptide corresponding to at least a ligand-binding portion of the extracellular domain of TLR9. In most instances a TLR9 ligand will also induce TLR9 signaling when contacted with TLR9 under suitable conditions. TLR9 signaling refers to TLR/IL-1R signal transduction mediated through the TLR9, as described in further detail elsewhere herein. As mentioned above, CpG nucleic acids have been reported to be TLR9 ligands, but TLR9 ligands may include other entities as well, including, for example, small molecules. As also previously mentioned, there appears to be a species-specific preference for at least certain TLR9s and certain CpG motifs. As used herein, a species-preferred CpG DNA refers to a particular CpG DNA that is optimized for signal induction by a TLR9 of a particular species. A CpG DNA that is optimized for signal induction by a TLR9 of a particular species refers to a CpG DNA having a sequence that preferentially binds to and/or induces signaling by TLR9 of that species. For example, a human-preferred CpG DNA shall refer to a CpG DNA that optimally stimulates human TLR9 to signal through its TIR domain. Likewise, a murine-preferred CpG DNA

- 31 -

shall refer to a CpG DNA that optimally stimulates murine TLR9 to signal through its TIR domain. Examples of human-preferred and murine-preferred CpG DNA are ODN 2006 (SEQ ID NO:58) and 1668 (SEQ ID NO:60), respectively.

5 The binding and species specificity of TLR9s are believed to be influenced by key amino acids present in the extracellular domain of TLR9. Key amino acids in a TLR9 as used herein refer to those amino acids which contribute significantly to ligand binding and ligand specificity of a particular TLR9 polypeptide.

A "CpG nucleic acid" or a "CpG immunostimulatory nucleic acid" as used herein is a nucleic acid containing at least one unmethylated CpG dinucleotide (cytosine-guanine
10 dinucleotide sequence, i.e., "CpG DNA" or DNA containing a 5' cytosine followed by 3' guanine and linked by a phosphate bond) which activates a component of the immune system. The entire CpG nucleic acid can be unmethylated or portions may be unmethylated but at least the C of the 5' CG 3' must be unmethylated.

In one embodiment a CpG nucleic acid is represented by at least the formula:

15
$$5'\text{-N}_1\text{X}_1\text{CGX}_2\text{N}_2\text{-3'}$$

wherein X_1 and X_2 are nucleotides, N is any nucleotide, and N_1 and N_2 are nucleic acid sequences composed of from about 0-25 N's each. In some embodiments X_1 is adenine, guanine, or thymine and/or X_2 is cytosine, adenine, or thymine. In other embodiments X_1 is cytosine and/or X_2 is guanine.

20 Nucleic acids having modified backbones, such as phosphorothioate backbones, also fall within the class of immunostimulatory nucleic acids. U.S. Pat. Nos. 5,723,335 and 5,663,153 issued to Hutcherson, et al. and related PCT publication WO95/26204 describe immune stimulation using phosphorothioate oligonucleotide analogues. These patents describe the ability of the phosphorothioate backbone to stimulate an immune response in a
25 non-sequence specific manner.

An immunostimulatory nucleic acid molecule, including for example a CpG DNA, may be double-stranded or single-stranded. Generally, double-stranded molecules may be more stable *in vivo*, while single-stranded molecules may have increased activity. The terms "nucleic acid" and "oligonucleotide" refer to multiple nucleotides (i.e., molecules comprising
30 a sugar (e.g., ribose or deoxyribose) linked to a phosphate group and to an exchangeable organic base, which is either a substituted pyrimidine (e.g., cytosine (C), thymine (T) or uracil (U)) or a substituted purine (e.g., adenine (A) or guanine (G)) or a modified base. As

- 32 -

used herein, the terms "nucleic acid" and "oligonucleotide" refer to oligoribonucleotides as well as oligodeoxyribonucleotides. The terms shall also include polynucleosides (i.e., a polynucleotide minus the phosphate) and any other organic base-containing polymer. The terms "nucleic acid" and "oligonucleotide" also encompass nucleic acids or oligonucleotides with a covalently modified base and/or sugar. For example, they include nucleic acids having backbone sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 2' position and other than a phosphate group at the 5' position. Thus modified nucleic acids may include a 2'-O-alkylated ribose group. In addition, modified nucleic acids may include sugars such as arabinose instead of ribose. Thus the nucleic acids may be heterogeneous in backbone composition thereby containing any possible combination of polymer units linked together such as peptide-nucleic acids (which have amino acid backbone with nucleic acid bases). In some embodiments the nucleic acids are homogeneous in backbone composition.

The substituted purines and pyrimidines of the immunostimulatory nucleic acids include standard purines and pyrimidines such as cytosine as well as base analogs such as C-5 propyne substituted bases. Wagner RW et al. (1996) *Nat Biotechnol* 14:840-4. Purines and pyrimidines include but are not limited to adenine, cytosine, guanine, thymine, 5-methylcytosine, 2-aminopurine, 2-amino-6-chloropurine, 2,6-diaminopurine, hypoxanthine, and other naturally and non-naturally occurring nucleobases, substituted and unsubstituted aromatic moieties.

The immunostimulatory nucleic acid is a linked polymer of bases or nucleotides. As used herein with respect to linked units of a nucleic acid, "linked" or "linkage" means two entities are bound to one another by any physicochemical means. Any linkage known to those of ordinary skill in the art, covalent or non-covalent, is embraced. Such linkages are well known to those of ordinary skill in the art. Natural linkages, which are those ordinarily found in nature connecting the individual units of a nucleic acid, are most common. The individual units of a nucleic acid may be linked, however, by synthetic or modified linkages.

Whenever a nucleic acid is represented by a sequence of letters it will be understood that the nucleotides are in 5' to 3' (or equivalent) order from left to right and that "A" denotes adenine, "C" denotes cytosine, "G" denotes guanine, "T" denotes thymidine, and "U" denotes uracil unless otherwise noted.

- 33 -

Immunostimulatory nucleic acid molecules useful according to the invention can be obtained from natural nucleic acid sources (e.g., genomic nuclear or mitochondrial DNA or cDNA), or are synthetic (e.g., produced by oligonucleotide synthesis). Nucleic acids isolated from existing nucleic acid sources are referred to herein as native, natural, or isolated nucleic acids. The nucleic acids useful according to the invention may be isolated from any source, including eukaryotic sources, prokaryotic sources, nuclear DNA, mitochondrial DNA, etc. Thus, the term nucleic acid encompasses both synthetic and isolated nucleic acids.

The immunostimulatory nucleic acids can be produced on a large scale in plasmids, (see *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989) and separated into smaller pieces or administered whole. After being administered to a subject the plasmid can be degraded into oligonucleotides. One skilled in the art can purify viral, bacterial, eukaryotic, etc. nucleic acids using standard techniques, such as those employing restriction enzymes, exonucleases or endonucleases.

For use in the instant invention, the immunostimulatory nucleic acids can be synthesized *de novo* using any of a number of procedures well known in the art. For example, the β -cyanoethyl phosphoramidite method (Beaucage SL and Caruthers MH, *Tetrahedron Let* 22:1859 (1981)); nucleoside H-phosphonate method (Garegg et al., *Tetrahedron Let* 27:4051-4054 (1986); Froehler et al., *Nucl Acid Res* 14:5399-5407 (1986); Garegg et al., *Tetrahedron Let* 27:4055-4058 (1986); Gaffney et al., *Tetrahedron Let* 29:2619-2622 (1988)). These chemistries can be performed by a variety of automated oligonucleotide synthesizers available in the market.

The immunostimulatory nucleic acid may be any size of at least 6 nucleotides but in some embodiments are in the range of between 6 and 100 or in some embodiments between 8 and 35 nucleotides in size. Immunostimulatory nucleic acids can be produced on a large scale in plasmids. These may be administered in plasmid form or alternatively they can be degraded into oligonucleotides before administration.

A "stabilized immunostimulatory nucleic acid" shall mean a nucleic acid molecule that is relatively resistant to *in vivo* degradation (e.g., via an exo- or endo-nuclease). Stabilization can be a function of length or secondary structure. Nucleic acids that are tens to hundreds of kbs long are relatively resistant to *in vivo* degradation. For shorter nucleic acids, secondary structure can stabilize and increase their effect. For example, if the 3' end of an

- 34 -

oligonucleotide has self-complementarity to an upstream region, so that it can fold back and form a sort of stem loop structure, then the oligonucleotide becomes stabilized and therefore exhibits more activity.

Some stabilized immunostimulatory nucleic acids have a modified backbone. It has been demonstrated that modification of the oligonucleotide backbone provides enhanced activity of the immunostimulatory nucleic acids when administered *in vivo*. Nucleic acids, including at least two phosphorothioate linkages at the 5' end of the oligonucleotide and multiple phosphorothioate linkages at the 3' end, preferably 5, may provide maximal activity and protect the oligonucleotide from degradation by intracellular exo- and endo-nucleases. Other modified oligonucleotides include phosphodiester modified oligonucleotide, combinations of phosphodiester and phosphorothioate oligonucleotide, methylphosphonate, methylphosphorothioate, phosphorodithioate, and combinations thereof. Each of these combinations and their particular effects on immune cells is discussed in more detail in U.S. Pat. Nos. 6,194,388 and 6,207,646, the entire contents of which are incorporated herein by reference. It is believed that these modified oligonucleotides may show more stimulatory activity due to enhanced nuclease resistance, increased cellular uptake, increased protein binding, and/or altered intracellular localization. Both phosphorothioate and phosphodiester nucleic acids are active in immune cells.

Other stabilized immunostimulatory nucleic acids include: nonionic DNA analogs, such as alkyl- and aryl-phosphates (in which the charged phosphonate oxygen is replaced by an alkyl or aryl group), phosphodiester and alkylphosphotriesters, in which the charged oxygen moiety is alkylated. Oligonucleotides which contain diol, such as tetraethyleneglycol or hexaethyleneglycol, at either or both termini have also been shown to be substantially resistant to nuclease degradation.

Phosphorothioate nucleic acid molecules may be synthesized using automated techniques employing either phosphoramidate or H-phosphonate chemistries. Aryl- and alkyl-phosphonates can be made, e.g., as described in U.S. Pat. No. 4,469,863; and alkylphosphotriesters (in which the charged oxygen moiety is alkylated as described in U.S. Pat. No. 5,023,243 and European Patent No. 092,574) can be prepared by automated solid phase synthesis using commercially available reagents. Methods for making other DNA backbone modifications and substitutions have been described. Uhlmann E and Peyman A (1990) *Chem Rev* 90:544; Goodchild J (1990) *Bioconjugate Chem* 1:165.

- 35 -

Other sources of immunostimulatory nucleic acids useful according to the invention include standard viral and bacterial vectors, many of which are commercially available. In its broadest sense, a "vector" is any nucleic acid material which is ordinarily used to deliver and facilitate the transfer of nucleic acids to cells. The vector as used herein may be an empty
 5 vector or a vector carrying a gene which can be expressed. In the case when the vector is carrying a gene the vector generally transports the gene to the target cells with reduced degradation relative to the extent of degradation that would result in the absence of the vector. In this case the vector optionally includes gene expression sequences to enhance expression of the gene in target cells such as immune cells, but it is not required that the gene
 10 be expressed in the cell.

Nucleic acid-binding fragments of TLRs are believed to include the extracytoplasmic (extracellular) domain or subportions thereof, such as those which include at least an MBD motif, a CXXC motif, or both an MBD motif and a CXXC motif.

Both mouse and human TLR9 have an N-terminal extension of approximately 180
 15 amino acids compared to other TLRs. An insertion also occurs at amino acids 253-268, which is not found in TLRs 1-6 but is present in human TLR7 and human TLR8. This insert has two CXXC motifs which participate in forming a CXXC domain. The CXXC domain resembles a zinc finger motif and is found in DNA-binding proteins and in certain specific CpG binding proteins, e.g., methyl-CpG binding protein-1 (MBD-1). Fujita N et al. (2000)
 20 *Mol Cell Biol* 20:5107-18. Both human and mouse TLR9 CXXC domains occur at aa 253-268:

CXXC motif:	GNCXXCXXXXXXXXXXCXXC	SEQ ID NO:62
Human TLR9:	GNCRRCDHAPNPCMEC	SEQ ID NO:63
25 Murine TLR9:	GNCRRCDHAPNPCMIC	SEQ ID NO:64

An additional motif believed to be involved in CpG binding is the MBD motif, also found in MBD-1, listed below as SEQ ID NO:53. Fujita, N et al.(2000) *Mol Cell Biol* 20:5107-18; Ohki I et al. (1999) *EMBO J* 18:6653-61. Amino acids 524-554 of hTLR9 and
 30 aa 525-555 of mTLR9 correspond to the MBD motif of MBD-1 as shown:

MBD motif:

- 36 -

	MBD-1	R-XXXXXXX-R-X-D-X-Y-XXXXXXXXX-R-S-XXXXXX-Y	SEQ ID NO:65
	hTLR9	Q-XXXXXXX-K-X-D-X-Y-XXXXXXXXX-R-L-XXXXXX-Y	SEQ ID NO:66
	mTLR9	Q-XXXXXXX-K-X-D-X-Y-XXXXXXXXX-Q-L-XXXXXX-Y	SEQ ID NO:67
5	hTLR9	Q-VLDLSRN-K-L-D-L-Y-HEHSFTELP-R-L-EALDLS-Y	SEQ ID NO:68
	mTLR9	Q-VLDLSHN-K-L-D-L-Y-HWKSFSLEP-Q-L-QALDLS-Y	SEQ ID NO:69

Although the signaling functions of MBD-1 and TLR9 are quite different, the core D-X-Y is conserved and is believed to be involved in CpG binding.

10 According to another aspect of the invention, a screening method is provided for identifying an immunostimulatory compound. The method according to this aspect of the invention involves contacting a functional TLR9 with a test compound; detecting presence or absence of a response mediated by a TLR9 signal transduction pathway in the presence of the test compound arising as a result of an interaction between the functional TLR9 and the test
15 compound; and determining the test compound is an immunostimulatory compound when the presence of a response mediated by the TLR9 signal transduction pathway is detected.

An immunostimulatory compound is a natural or synthetic compound that is capable of inducing an immune response when contacted with an immune cell. A TLR9 ligand that is an immunostimulatory compound is a natural or synthetic compound that is capable of
20 inducing an immune response when contacted with an immune cell that expresses TLR9. A TLR9 ligand that is an immunostimulatory compound is also a natural or synthetic compound that is capable of inducing a TLR/IL-1R signal transduction pathway when contacted with a TLR9. Immunostimulatory compounds include but are not limited to immunostimulatory
25 molecule, polynucleotide or oligonucleotide, a polypeptide or oligopeptide, a lipid or lipopolysaccharide, a small molecule.

A basis for certain of the screening assays is the presence of a functional TLR9 in a cell. The functional TLR9 in some instances is naturally expressed by a cell. In other instances, expression of the functional TLR9 can involve introduction or reconstitution of
30 species-specific TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact with an

- 37 -

immunostimulatory nucleic acid. In yet other instances, expression of the functional TLR9 can involve introduction of a chimeric or modified TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact
5 with an immunostimulatory nucleic acid. Examples of cell lines lacking TLR9 or immunostimulatory nucleic acid responsiveness include, but are not limited to, 293 fibroblasts (ATCC CRL-1573), MonoMac-6, THP-1, U937, CHO, and any TLR9 knock-out. The introduction of the species-specific, chimeric or modified TLR9 into the cell or cell line is preferably accomplished by transient or stable transfection of the cell or cell line with a
10 TLR9-encoding nucleic acid sequence operatively linked to a gene expression sequence (as described above). Methods for transient and for stable transfection of a cell are well known in the art.

The screening assays can have any of a number of possible readout systems based upon either TLR/IL-1R signaling pathway or other assays useful for assessing response to
15 immunostimulatory nucleic acids. It has been reported that immune cell activation by CpG immunostimulatory sequences is dependent in some way on endosomal processing.

In certain embodiments, the readout for the screening assay is based on the use of native genes or, alternatively, cotransfected or otherwise co-introduced reporter gene constructs which are responsive to the TLR/IL-1R signal transduction pathway involving
20 MyD88, TRAF, p38, and/or ERK. Häcker H et al. (1999) *EMBO J* 18:6973-6982. These pathways activate kinases including κ B kinase complex and c-Jun N-terminal kinases. Thus reporter genes and reporter gene constructs particularly useful for the assays can include a reporter gene operatively linked to a promoter sensitive to NF- κ B. Examples of such promoters include, without limitation, those for NF- κ B, IL-1 β , IL-6, IL-8, IL-12 p40, CD80,
25 CD86, and TNF- α . The reporter gene operatively linked to the TLR-sensitive promoter can include, without limitation, an enzyme (e.g., luciferase, alkaline phosphatase, β -galactosidase, chloramphenicol acetyltransferase (CAT), etc.), a bioluminescence marker (e.g., green-fluorescent protein (GFP, U.S. Pat. No. 5,491,084), blue fluorescent protein, etc.), a surface-expressed molecule (e.g., CD25), and a secreted molecule (e.g., IL-8, IL-12 p40, TNF- α). In
30 certain embodiments the reporter is selected from IL-8, TNF- α , NF- κ B-luciferase (NF- κ B-luc; Häcker H et al. (1999) *EMBO J* 18:6973-6982), IL-12 p40-luc (Murphy TL et al. (1995)

- 38 -

Mol Cell Biol 15:5258-5267), and TNF-luc (Häcker H et al. (1999) *EMBO J* 18:6973-6982). At least one of these reporter constructs (NF- κ B-luc) is commercially available (Stratagene, La Jolla, CA). In assays relying on enzyme activity readout, substrate can be supplied as part of the assay, and detection can involve measurement of chemiluminescence, fluorescence, color development, incorporation of radioactive label, drug resistance, or other marker of enzyme activity. For assays relying on surface expression of a molecule, detection can be accomplished using FACS analysis or functional assays. Secreted molecules can be assayed using enzyme-linked immunosorbent assay (ELISA) or bioassays. Many such readout systems are well known in the art and are commercially available.

10 According to one embodiment of this method, comparison can be made to a reference immunostimulatory nucleic acid. The reference immunostimulatory nucleic acid may be any suitably selected immunostimulatory nucleic acid, including a CpG nucleic acid. In certain embodiments the screening method is performed using a plurality of test nucleic acids. In certain embodiments comparison of test and reference responses is based on comparison of quantitative measurements of responses in each instance.

15 In another aspect the invention provides a screening method for identifying species specificity of an immunostimulatory nucleic acid. The method involves contacting a TLR9 of a first species with a test immunostimulatory nucleic acid; contacting a TLR9 of a second species with the test immunostimulatory nucleic acid; measuring a response mediated by a TLR signal transduction pathway associated with the contacting the TLR9 of the first species with the test immunostimulatory nucleic acid; measuring a response mediated by the TLR signal transduction pathway associated with the contacting the TLR9 of the second species with the test immunostimulatory nucleic acid; and comparing the two responses. The TLR9 may be expressed by a cell or it may be part of a cell-free system. The TLR9 may be part of a complex, with either another TLR or with another protein, e.g., MyD88, IRAK, TRAF, I κ B, NF- κ B, or functional homologues and derivatives thereof. Thus for example a given ODN can be tested against a panel of human fibroblast 293 fibroblast cells transfected with TLR9 from various species and optionally cotransfected with a reporter construct sensitive to TLR/IL-1R activation pathways. Thus in another aspect, the invention provides a method for screening species selectivity with respect to a given nucleic acid sequence.

30 Test compounds can include but are not limited to peptide nucleic acids (PNAs), antibodies, polypeptides, carbohydrates, lipids, hormones, and small molecules. Test

- 39 -

compounds can further include variants of a reference immunostimulatory nucleic acid incorporating any one or combination of the substitutions described above. Test compounds can be generated as members of a combinatorial library of compounds.

In preferred embodiments, the screening methods can be performed on a large scale and with high throughput by incorporating, e.g., an array-based assay system and at least one automated or semi-automated step. For example, the assays can be set up using multiple-well plates in which cells are dispensed in individual wells and reagents are added in a systematic manner using a multiwell delivery device suited to the geometry of the multiwell plate. Manual and robotic multiwell delivery devices suitable for use in a high throughput screening assay are well known by those skilled in the art. Each well or array element can be mapped in a one-to-one manner to a particular test condition, such as the test compound. Readouts can also be performed in this multiwell array, preferably using a multiwell plate reader device or the like. Examples of such devices are well known in the art and are available through commercial sources. Sample and reagent handling can be automated to further enhance the throughput capacity of the screening assay, such that dozens, hundreds, thousands, or even millions of parallel assays can be performed in a day or in a week. Fully robotic systems are known in the art for applications such as generation and analysis of combinatorial libraries of synthetic compounds. See, for example, U.S. Pat. Nos. 5,443,791 and 5,708,158.

The following examples are provided for illustrative purposes and are not meant to be limiting in any way.

Examples

Example 1. Cloning and Sequencing of Rat, Porcine, Bovine, Equine, Ovine, Canine, and Feline TLR9

Cells and Tissues. Lymphoid tissues, primarily spleen or blood mononuclear cells (PBMC) from five mammalian species were collected: mouse, pig, bovine, rat and horse. Spleen samples were collected in RNeasyTM (Ambion[®], Austin, TX, USA), stabilized at 4°C overnight and stored at -70°C. Blood samples were centrifuged at 500 x g for 25 min at room temperature and the buffy coat, containing enriched PBMC, was then removed and stored at -70°C. The mouse specimen was used as a comparative positive control.

- 40 -

First-strand cDNA synthesis. Total RNA from the spleen and PBMC samples was isolated using a monophasic solution of phenol and guanidine isothiocyanate: TRIzol™ reagent (GIBCO BRL®, Burlington, ON, Canada) according to the manufacturer's instructions. First-strand cDNA was synthesized from the total RNA using
5 SUPERScript™ II reverse transcriptase (GIBCO BRL®, Burlington, ON, Canada). Approximately 3 µg of total RNA was added to 50 pmoles of oligo(dT) primer [poly T₍₁₈₎]; the mixture was heated to 70°C for 10 min and subsequently chilled on ice. The following was added to the cooled reaction mixture: 1 µl of mixed dNTP stock containing 10 mM each dATP, dCTP, dGTP and dTTP (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) at
10 neutral pH, 1X first strand buffer (50 mM Tris-HCl pH 8.3/ 75 mM KCl/ 3 mM MgCl₂) and 2 µl of 0.1 M DTT. The mixture was subsequently heated to 42°C for 2 min, followed by addition of 200 units of SUPERScript™ II reverse transcriptase. The reaction was carried out at 42°C for 50 min, followed by 70°C for 15 min. The first-strand cDNA was used as the template for subsequent polymerase chain reaction (PCR) amplifications.

15 *PCR amplification.* TLR9 gene was PCR amplified from each of the above-mentioned species using primers designed from known mouse and human TLR9 sequence in Genbank: Accession AF314224 and AF259262, respectively. The primers were designed using the primer design software, Clone Manager 5 (Scientific and Educational Software, Durham, NC, USA). TLR9 gene-specific primers used were:

20 forward primer 5'-ACCTTGCCCTGCCTTCCTACCCTGTGA-3' (SEQ ID NO:37) and reverse primer 5'-GTCCGTGTGGGCCAGCACAAA-3' (SEQ ID NO:38).

The 2.7 Kbp fragment was PCR amplified using Advantage® 2 DNA polymerase mix (BD Biosciences Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. PCR reaction volumes of 25 µl contained 15 pmoles of each primer, 0.2 mM of dNTP mix
25 and 1 µl of reverse transcription reaction. PCR amplification was conducted by initial denaturation at 94°C for 1 min followed by 30 cycles of 94°C denaturation (15 sec), 65°C annealing (45 sec) and 72°C extensions (2 min), with a final extension at 72°C for 5 min.

Cloning and sequencing. The PCR amplified fragment was treated with 500 units of T4 DNA polymerase (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) for 15 min
30 at room temperature prior to cleaning the reaction with QIAquick PCR purification kit (QIAGEN Inc., Mississauga, ON, Canada). The fragment was then ligated to pZErO™ - 2

- 41 -

vector (Invitrogen™ Life Technologies, Burlington, ON, Canada), treated with *Eco RV* restriction enzyme, using T4 DNA Ligase (GIBCO BRL®, Burlington, ON, Canada). *E. coli* TOP 10 chemically competent cells (Invitrogen™ Life Technologies, Burlington, ON, Canada) were used to transform ligated products. Plasmids containing the 2.7 Kbp fragment were sequenced using an automated DNA sequencer, CEQ™ 2000XL DNA analysis system (Beckman Coulter Inc., Fullerton, CA, USA).

Sequences of the 2.7 Kbp fragment were derived from three clones of each species selected from independent PCR reactions to account for errors that may have been incurred during the PCR amplifications and to confirm the sequence data.

Nucleotide sequences of the rat, porcine, bovine, equine, ovine, canine, and feline TLR9 were extended and completed using standard 5' and 3' RACE PCR and primers designed using the sequences obtained from the 2.7 Kbp fragments.

Results. Nucleotide sequences of rat, porcine, bovine, equine, canine, and feline TLR9 cDNA obtained by the methods above are provided as SEQ ID NOs 3, 7, 11, 15, 19, 23, and 27, respectively. Deduced amino acid sequences are provided as SEQ ID NOs 1, 5, 9, 13, 17, 21, and 25, respectively. Deduced amino acid sequences of full-length murine and human TLR9 are provided as SEQ ID NOs 29 and 33, respectively.

Example 2. Comparison of Aligned Sequences for TLR9 from Various Mammalian Species.

Multiple sequence alignment of deduced amino acid sequences for feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 polypeptides was performed using Clustal W 1.82 (see, for example, www.cmbi.kun.nl/bioinf/tools/clustalw.shtml). In addition, paired sequence alignment of deduced amino acid sequences for murine and human TLR9 polypeptides was performed using Clustal W 1.82. The results of the multiple sequence alignment are presented in **Figure 1**. As will be appreciated from Figure 1, certain amino acids are highly conserved across all species examined. Similarly, certain amino acids differ only by conservative amino acid substitutions among the various species. In addition, it is evident that certain amino acids which are conserved between murine and human TLR9 are not conserved in other species. Furthermore, Figure 1 also indicates that certain amino acids are highly divergent across various species. The information provided by the comparison of multiple species adds significantly to the information available by comparison between only murine and human TLR9 sequences.

- 42 -

The putative transmembrane regions of the TLR9 polypeptides are indicated in boxes in Figure 1. Sequence upstream of each transmembrane region is extracellular domain and is believed to include sequence primarily responsible for binding to TLR9 ligands, including CpG DNA. The extracellular domains of feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 correspond to amino acids numbered 1-820, 1-822, 1-818, 1-821, 1-818, 1-819, 1-820, 1-820, and 1-821, respectively, as shown in Figure 1.

Figure 2 presents an evolutionary relatedness tree for six TLR9 polypeptides examined. The cladogram in Figure 2 was prepared using Clustal W (see above). As can be appreciated from this figure, murine and human TLR9 are nearly the most divergent TLR9s in this group. Surprisingly, human and horse TLR9 appear relatively closely related.

Example 3. Reconstitution of TLR9 Signaling in 293 Fibroblasts.

Mouse TLR9 cDNA (SEQ ID NO:31) and human TLR9 cDNA (SEQ ID NO:35) in pT-Adv vector (from Clontech) were individually cloned into the expression vector pcDNA3.1(-) from Invitrogen using the EcoRI site. Utilizing a "gain of function" assay it was possible to reconstitute human TLR9 (hTLR9) and murine TLR9 (mTLR9) signaling in CpG-DNA non-responsive human 293 fibroblasts (ATCC, CRL-1573). The expression vectors mentioned above were transfected into 293 fibroblast cells using the calcium phosphate method.

Since NF- κ B activation is central to the IL-1/TLR signal transduction pathway (Medzhitov R et al. (1998) *Mol Cell* 2:253-258; Muzio M et al. (1998) *J Exp Med* 187:2097-101), cells were transfected with hTLR9 or co-transfected with hTLR9 and an NF- κ B-driven luciferase reporter construct. Human fibroblast 293 cells were transiently transfected with hTLR9 and a six-times NF- κ B-luciferase reporter plasmid (NF- κ B-luc) or with hTLR9 alone. After stimulus with CpG-ODN (2006, 2 μ M, TCGTCGTTTTGTCTGTTTTGTCTGTT, SEQ ID NO:58), GpC-ODN (2006-GC, 2 μ M, TGCTGCTTTTGTGCTTTTGTGCTT, SEQ ID NO:59), LPS (100 ng/ml) or media, NF- κ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results representative of three independent experiments showed that cells expressing hTLR9 responded to CpG-DNA but not to LPS.

Independently, human fibroblast 293 cells were transiently transfected with mTLR9 and the NF- κ B-luc construct or with mTLR9 alone. After stimulation with CpG-ODN (1668, 2 μ M; TCCATGACGTTTCCTGATGCT, SEQ ID NO:60), GpC-ODN (1668-GC, 2 μ M;

- 43 -

TCCATGAGCTTCCTGATGCT, SEQ ID NO:61), LPS (100 ng/ml) or media, NF- κ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results showed that expression of TLR9 (human or mouse) in 293 cells results in a gain of function for CpG-DNA stimulation.

5 To generate stable clones expressing human TLR9, murine TLR9, or either TLR9 with the NF- κ B-luc reporter plasmid, 293 cells were transfected in 10 cm plates (2×10^6 cells/plate) with 16 μ g of DNA and selected with 0.7 mg/ml G418 (PAA Laboratories GmbH, Cölbe, Germany). Clones were tested for TLR9 expression by RT-PCR. The clones were also screened for IL-8 production or NF- κ B-luciferase activity after stimulation with
10 ODN. Four different types of clones were generated.

293-hTLR9-luc:	expressing human TLR9 and 6-fold NF- κ B-luciferase reporter
293-mTLR9-luc:	expressing murine TLR9 and 6-fold NF- κ B-luciferase reporter
293-hTLR9:	expressing human TLR9
15 293-mTLR9:	expressing murine TLR9

Results indicated that stable clones also responded to CpG-ODN.

Example 4. Similar ODN Sequence Specificity of TLR9 of Human and Equine TLR9.

20 3×10^6 293T cells were electroporated with 5 μ g NF- κ B-luc plasmid and 5 μ g of either horse TLR9-pcDNA3.1 plasmid or humanTLR9-pcDNA3.1 plasmid at 200V, 975 μ F. After the electroporation the cells were plated in 96-well cell culture plates at 2.5×10^4 cells per well and grown overnight at 37°C. The cells were stimulated with the indicated concentration of ODN for 16h, after which the supernatant was removed and the cells lysed in lysis buffer and
25 frozen for at least 2 hours at -80°C. Luciferase activity was measured by adding Luciferase Assay substrate from Promega. Values are given as fold specific induction over non-stimulated control. Results are shown in Figure 3.

As shown in Figure 3, ODN 2006 (TCGTCGTTTTGTCGTTTTGTCGTT; SEQ ID NO:58) has a strong specificity for human TLR9. ODN 1982
30 (TCCAGGACTTCTCTCAGGTT; SEQ ID NO:70) was the negative control ODN. ODN 5890 (TCCATGACGTTTTTGATGTT; SEQ ID NO:39) has a strong specificity for mouse

- 44 -

TLR9. This experiment demonstrates the similarity of horse TLR9 to human TLR9 in binding specificity, a result predicted by the evolutionary relatedness of horse TLR9 to human TLR9. Mouse TLR9 is more distant from horse TLR9 and human TLR9 in sequence homology, and ODN 5890 was not detected by either human or horse TLR9.

5

Example 5. Non-human, Non-murine Native Mammalian TLR9 Useful in Screening for Human-Preferred CpG DNA.

Native rat, porcine, bovine, equine, and ovine TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Rat, porcine, bovine, equine, or ovine TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

20 Example 6. Chimeric TLR9 Useful in Screening for Human-Preferred CpG DNA.

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

30

Example 7. Chimeric TLR9 Responsive to Both Human-Preferred and Murine-Preferred CpG DNA.

- 45 -

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006) and also screened for binding or TLR9 signaling activity when contacted with murine-preferred CpG DNA (ODN 1668). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in each of these assays are then used as the basis for screening for additional human-preferred CpG DNA and for screening for additional murine-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA or candidate murine-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA. Candidate murine-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as murine-preferred CpG DNA.

Equivalents

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by examples provided, since the examples are intended as a single illustration of one aspect of the invention and other functionally equivalent embodiments are within the scope of the invention. Various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims. The advantages of the invention are not necessarily encompassed by each embodiment of the invention.

All references, patents and patent publications that are recited in this application are incorporated in their entirety herein by reference.

We claim:

- 46 -

Claims

1. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.
5
2. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.
3. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a
10 polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.
4. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ
15 ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.
5. A vector comprising the nucleic acid of any of claims 3-4.
6. A cell comprising the vector of claim 5.
20
7. An antibody or fragment thereof that binds specifically to the polypeptide of any of claims 1-2.
8. A method for identifying key amino acids in a TLR9 of a first species which
25 confer specificity for CpG DNA optimized for TLR9 of the first species, comprising:
aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species;
30 generating an initial set of candidate amino acids in the TLR9 of the first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the

- 47 -

TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with
5 the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

10 9. A method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9, comprising:

aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a
15 CpG DNA optimized for murine TLR9;

generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the
20 initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids.

25

10. The method according to claim 9, performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight, said weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred
30 CpG DNA).

- 48 -

11. An isolated polypeptide comprising an amino acid sequence identical to SEQ ID NO:30 except for substitution of at least one key amino acid identified according to the method of any of claims 9 or 10.

5 12. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide according to claim 11.

13. A vector comprising the nucleic acid of claim 12.

10 14. A cell comprising the vector of claim 13.

15. An antibody that binds specifically to the polypeptide of claim 14.

16. A screening method to identify a TLR9 ligand, comprising:
15 contacting a polypeptide according to any of claims 1, 2, or 11 with a candidate TLR9 ligand;
 measuring a signal in response to the contacting; and
 identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling.

20 17. The method of claim 16, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

18. The method of claim 17, wherein the reporter gene is operatively linked to a
25 promoter sensitive to NF- κ B.

19. The method of claim 17, wherein the candidate TLR9 ligand is an immunostimulatory nucleic acid.

30 20. The method of claim 19, wherein the immunostimulatory nucleic acid is CpG DNA.

- 49 -

21. A screening method to identify species-specific CpG-motif preference of an isolated polypeptide of claim 2 or claim 11, comprising:

contacting an isolated polypeptide of claim 2 or claim 11 with a CpG DNA comprising a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GCGGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG;

measuring a signal in response to the contacting; and

identifying a species-specific CpG-motif preference when the signal in response to the contacting is consistent with TLR9 signaling.

22. The method of claim 21, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

23. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF- κ B.

24. The method of claim 21, wherein the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

20	TCCATGACGTTTTTGATGTT	(SEQ ID NO:39),
	TCCATAACGTTTTTGATGTT	(SEQ ID NO:40),
	TCCATCACGTTTTTGATGTT	(SEQ ID NO:41),
	TCCATTACGTTTTTGATGTT	(SEQ ID NO:42),
	TCCATGGCGTTTTTGATGTT	(SEQ ID NO:43),
25	TCCATGCCGTTTTTGATGTT	(SEQ ID NO:44),
	TCCATGTCGTTTTTGATGTT	(SEQ ID NO:45),
	TCCATGATGTTTTTGATGTT	(SEQ ID NO:46),
	TCCATGAAGTTTTTGATGTT	(SEQ ID NO:47),
	TCCATGAGGTTTTTGATGTT	(SEQ ID NO:48),
30	TCCATGACATTTTTGATGTT	(SEQ ID NO:49),
	TCCATGACCTTTTTGATGTT	(SEQ ID NO:50),
	TCCATGACTTTTTTGATGTT	(SEQ ID NO:51),
	TCCATGACGCTTTTGATGTT	(SEQ ID NO:52),
	TCCATGACGATTTTGATGTT	(SEQ ID NO:53),
35	TCCATGACGGTTTTGATGTT	(SEQ ID NO:54),
	TCCATGACGTCTTTGATGTT	(SEQ ID NO:55),
	TCCATGACGTATTTGATGTT	(SEQ ID NO:56), and
	TCCATGACGTGTTTGATGTT	(SEQ ID NO:57).

Figure 1 (1/3)

```

feline      MGPCHGALHPLSLVQAAALAVALAQGTLPAPFLPCELQPHGLVNCNWLFLKSVPHFSAAA 60
canine      MGPCRGALHPLSLVQAAALALALAQGTLPAPFLPCELQPHGLVNCNWLFLKSVPRFSAAA 60
bovine      MGP-YCAPHPLSLVQAAALAAALAEGLTPAPFLPCELQPHGQVDCNWLFLKSVPHFSAGA 59
mouse       MGP-YCAPHPLSLVQAAALAAALAEGLTPAPFLPCELQPHGQVDCNWLFLKSVPHFSAGA 59
ovine       MGP-YCAPHPLSLVQAAALAAALAEGLTPAPFLPCELQPHGQVDCNWLFLKSVPHFSAGA 59
porcine     MGP-RCTLHPLSLVQVTTALAAALAQGTLPAPFLPCELQPHGLVNCNWLFLKSVPHFSAAA 59
horse       MGPCHGALQPLSLVQAAALAVALAQGTLPAPFLPCELQPHGLVNCNWLFLKSVPHFSAAA 60
human       MGFCRSALHPLSLVQAIMLMTLALGTLPAPFLPCELQPHGLVNCNWLFLKSVPHFSMAA 60
rat         MVLCRRTLHPLSLVQAAVLAALALGTLPAPFLPCELKPHGLVDCNWLFLKSVPHFSAAE 60
*           : :*****. ** : * * * *.*****: ; * * :*****:*** .

feline      PRGNVTSLSLSYNSRIHHLHDSDFVHLSSLRRLNLKWNCPASLSPMHFPCMTIEPHTFL 120
canine      PRGNVTSLSLSYNSRIHHLHDYDFVHFVHLRRLNLKWNCPASLSPMHFPCMTIEPNTFL 120
bovine      PRANVTSLSLSISNRIHHLHDSDFVHLNLRVNLKWNCPAGLSPMHFPCMTIEPNTFL 119
mouse       PRANVTSLSLSISNRIHHLHDSDFVHLNLRVNLKWNCPAGLSPMHFPCMTIEPNTFL 119
ovine       PRANVTSLSLSISNRIHHLHDSDFVHLNLRVNLKWNCPAGLSPMHFPCMTIEPNTFL 119
porcine     PRANVTSLSLSISNRIHHLHDSDFVHLNLRVNLKWNCPAGLSPMHFPCMTIEPNTFL 119
horse       PRDNVTSLSLSISNRIHHLHDSDFVHLNLRVNLKWNCPAGLSPMHFPCMTIEPNTFL 120
human       PRGNVTSLSLSISNRIHHLHDSDFVHLNLRVNLKWNCPAGLSPMHFPCMTIEPNTFL 120
rat         PRSNITSLSLSIANRIHHLHDLDFVHLNVRQLNLKWNCPAGLSPMHFPCMTIEPKTFL 120
** *.***** :*****: **.:: :. ***** .***:*.**:***** ***

feline      AVPTLEELNLSYNSITVTPALPSSLSVLSLSRTNIVLDPANLAGLSLRFLELDGNCYY 180
canine      AVPTLEELNLSYNSITVTPALPSSLSVLSLSRTNIVLDPATLAGLYALRFLELDGNCYY 180
bovine      AVPTLEELNLSYNGITVTPALPSSLSVLSLSHTSILVLGPTHFTGLHALRFLYMDGNCYY 179
mouse       AVPTLEELNLSYNGITVTPALPSSLSVLSLSHTSILVLGPTHFTGLHALRFLYMDGNCYY 179
ovine       AVPTLEELNLSYNGITVTPALPSSLSVLSLSHTSILVLGPTHFTGLHALRFLYMDGNCYY 179
porcine     AVPTLEELNLSYNSITVTPALPSSLSVLSLSRTNIVLDPHTLGLHALRFLYMDGNCYY 179
horse       AVPTLEELNLSYNGITVTPALPSSLSVLSLSHTSILVLGPTHFTGLHALRFLYMDGNCYY 180
human       AVPTLEELNLSYNNITVTPALPKSLISLSLSHTNIMLDSASLAGLHALRFLFMDGNCYY 180
rat         AMRMLEELNLSYNGITVTPRLPSSLTNLSLSHTNIVLDASSLAGLSLRFLELDGNCYY 180
*: ** :*****. * *** **.*. * ** :*.** *..: :***:*** **:*****

feline      KNPCPQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYLLSYNHIITLAPEDL 240
canine      KNPCQQALQVAPGALLGLGNLTHLSLKYNNTVVPRLPPSLEYLLSYNHIITLAPEDL 240
bovine      MNPCPRALEVAPGALLGLGNLTHLSLKYNNTLTPVPRRLPPSLDTLLSYNHIVTLAPEDL 239
mouse       MNPCPRALEVAPGALLGLGNLTHLSLKYNNTLTPVPRRLPPSLDTLLSYNHIVTLAPEDL 239
ovine       KNPCQQAQVAPGALLGLGNLTHLSLKYNNTLTPVPRRLPPSLDTLLSYNHIITLAPEDL 239
porcine     KNPCQGALEVPVAPGALLGLGNLTHLSLKYNNTLTPVPRRLPPSLETLLSYNHIVTLAPEDL 239
horse       KNPCGRALEVAPGALLGLGNLTHLSLKYNNTLTPVPRRLPPSLEYLLSYNHIVTLAPEDL 240
human       KNPCQRALEVAPGALLGLGNLTHLSLKYNNTLTPVPRRLPPSLEYLLSYNRIKVLAPEDL 240
rat         KNPCNGAVNVTDAFLGLSNLTHLSLKYNNTLTPVPRRLPPSLEYLLSYNLIVKGAEDL 240
*** *:.*.*.***.***** ***** ** **.*: ***** *:.*.***

feline      ANLTALRVLDVGGNCRRCDHARNPCMECPKGFPHLPDFTFSLHNLHLEGLVLKDSLSYLN 300
canine      ANLTALRVLDVGGNCRRCDHARNPCRECPKGFQHPNTFGLSHLEGLVLKDSLSYSLD 300
bovine      ANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDFTFSLSRLEGLVLKDSLSYKLE 299
mouse       ANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDFTFSLSRLEGLVLKDSLSYKLE 299
ovine       ANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDFTFSLSRLEGLVLKDSLSYKLE 299
porcine     ANLTALRVLDVGGNCRRCDHARNPCRECPKDHDPKLHSDFTFSLSRLEGLVLKDSLSYQNL 300
horse       ANLTALRVLDVGGNCRRCDHARNPCVECPKHFQHPDFTFSLSRLEGLVLKDSLSYQNL 300
human       ANLTALRVLDVGGNCRRCDHARNPCMECPRHFPQHPDFTFSLSRLEGLVLKDSLSYQNL 300
rat         ANLTSLRMLDVGGNCRRCDHAPDLCTECRQKSLDLHPQTFHHLHLEGLVLKDSLSYSLN 300
****.***:***** ***** : * ** : .***:*** **.:*****:***** *:

feline      PRWFHALGNLMVLDLSENFLYDCITKTTFQGLAQRLRLNLSFNHKKVSAFHLHLAPSF 360
canine      PRWFHGLGNLMVLDLSENFLYDCITKTTFQGLAQRLRLNLSFNHKKVSAFHLHLASSF 360
bovine      KDWFRGLGRLQVLDLSENFLYDYITKTTFNDLTQLRLRLNLSFNHKKVSAFHLHLASSF 359
mouse       KDWFRGLGRLQVLDLSENFLYDYITKTTFNDLTQLRLRLNLSFNHKKVSAFHLHLASSF 359
ovine       KDWFRGLGRLQVLDLSENFLYDYITKTTFNRNLTQLRLRLNLSFNHKKVSAFHLHLAPSF 359
porcine     TRWFRGLDRLQVLDLSENFLYDCITKTTFQGLARLRLNLSFNHKKVSAFHLHLAPSF 359
horse       PRWFRGLGNLTVLDLSENFLYDCITKTTFQGLAQRLRLNLSFNHKKVSAFHLHLAPSF 360
human       ASWFRGLGNLTVLDLSENFLYKCTKTTFQGLAQRLRLNLSFNHKKVSAFHLHLAPSF 360
rat         SKWFRGLANLTVLDLSENFLYKCTKTTFQGLAQRLRLNLSFNHKKVSAFHLHLAPSF 360
**:*.*.*****.***.*.***:***.*****.*****.*****.*****.***

```



```
feline      DLSDNRISGAMELAAATGEVDG--GERVRLPSGDLALGPPTPSSEGFMPGCKTLNFTLD 478
canine      DLSDNRISGAAPAAATGEVEADCGERVWPQSRDLALGPLTGPSEAFMPSCRTLNFTLD 480
bovine      DLSDNRISGAATPAAALGEVDS--RVEVWRLPRGLAPGPLDAVSSKDFMPSCN-LNFTLD 476
mouse       DLSDNRISGAATPAAALGEVDS--RVEVWRLPRGLAPGPLDAVSSKDFMPSCN-LNFTLD 476
ovine       DLSDNRISGAARPVAALGEVDS--GVEVWRWPRGLAPGPLAAVSAKDFMPSCN-LNFTLD 476
porcine     DLSDNRISGAARPVAITREVDG--RERVWLPSRNLAPRPLDTRSEDFMPNCKAFSFTLD 477
horse       DLSDNRISGAVEPVATTGEVDG--GKKVWLTSRDLTPGPLDTPSSEDFMPSCNLSFTLD 478
human       DLSDNRISGASELTATMGADG--GEKVWLQPGDLAPAPVDTPSSEDFRPNCSSTLNFTLD 478
rat         DLSDNRISGPPTLSRVAPEKAD-EAEKGVPWPASLTALPSTPVSKNFVMRCKNLRFMTD 479
***-*****          *                               *:          *:          *:          *:          *
```

[illegible]

feline	SLRALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNRHLTLLPRTLNDNLPKSLRL	658
canine	SLRALDFSGNTLSQMWAEGDLYLRFFQGLRSLVQLDLSQNRHLTLLPRNLNDNLPKSLRL	660
bovine	SLRALDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSENHLTLLPRHLNDNLPKSLRQL	656
mouse	SLRALDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSENHLTLLPRHLNDNLPKSLRQL	656
ovine	SLRALDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSKNHLTLLPRHLNDNLPKSLRQL	656
porcine	SLCALDFSGNDLSRMWAEGDLYLRFFQGLRSLVWLDLSQNHHLTLLPRALNDNLPKSLKHL	657
horse	SLWALDFSGNSLSQMWAEGDLYLRFFQGLRSLIRLDLSQNRHLTLLPCTLGNLPKSLQLL	658
human	SLRALDFSGNALGHMWAEGDLYLHFFQGLSGLIWL DLSQNRHLTLLPQTLRNLPKSLQVL	658
rat	SVEYLD FSGNGVGRMDEEDLYLYFFQDLRSLIHLDLSQNKHLIRLPQNLYLPKSLTKL	659
	*. ***** :.*. :.***** :.*. :.***** :.*. :.***** *	

[illegible]

Figure 2

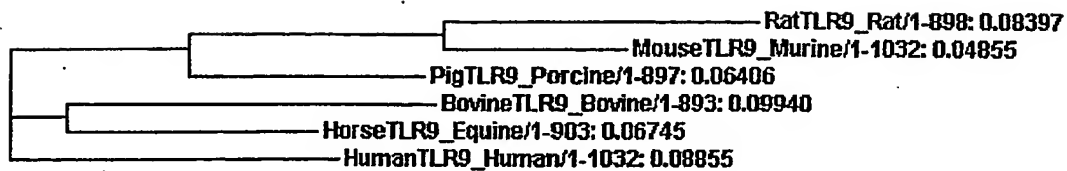
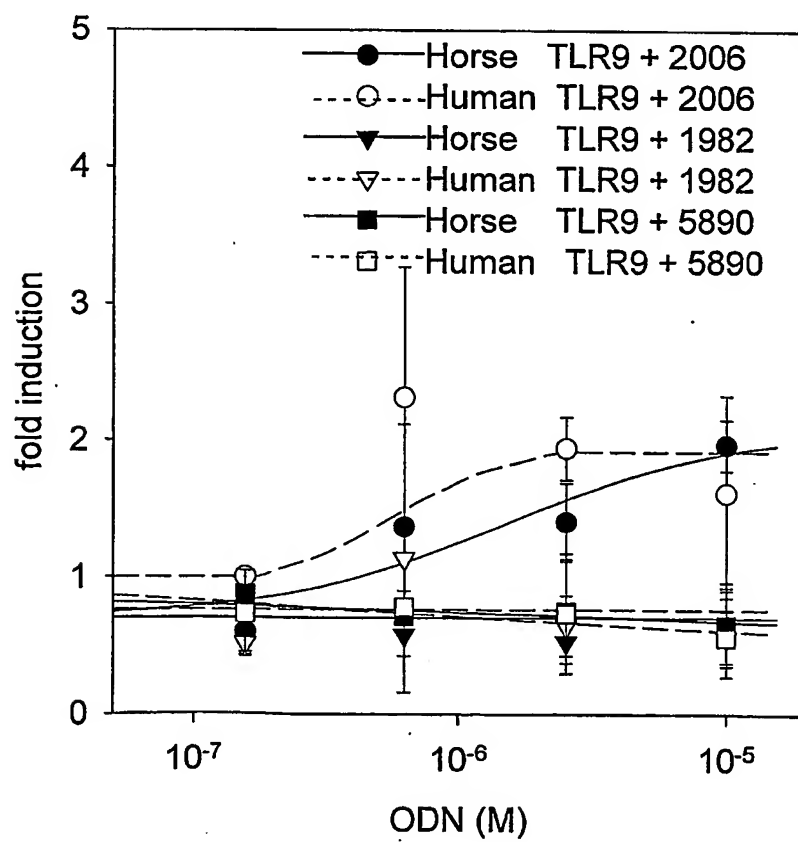


Figure 3



SEQUENCE LISTING

<110> Coley Pharmaceutical GmbH
University of Saskatchewan
Qiagen GmbH

<120> TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

<130> C1041.70040WO00

<150> US 60/412,479

<151> 2002-09-19

<160> 70

<170> PatentIn version 3.1

<210> 1

<211> 1032

<212> PRT

<213> Rattus norvegicus

<400> 1

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn
50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn
65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met
100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
130 135 140

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
 145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro
 180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser
 260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe
 290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu
 325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala
 340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu
 355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu
 370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala
 405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr
 420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val
 435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser
 450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu
 465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
 485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala
 500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp
 515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu
 530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
 545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser
 565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val
 580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly
 595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe

610	615	620
Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys		
625	630	635 640
Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu		
	645	650 655
Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser		
	660	665 670
Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn		
	675	680 685
Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu		
	690	700
Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala		
705	710	715 720
Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn		
	725	730 735
Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn		
	740	745 750
Leu Thr Val Leu Asp Val Ser Ser Asn Pro Leu His Cys Ala Cys Gly		
	755	760 765
Ala Pro Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly		
	770	775 780
Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Arg Gln Leu Gln Gly Arg		
785	790	795 800
Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Asp Val Leu Ser		
	805	810 815
Arg Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Thr Val		
	820	825 830
Leu Pro Leu Leu Gln His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe		
	835	840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Thr Arg Gly Arg Arg Ser
 850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln
 865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu
 885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp
 900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr
 915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Lys Val Ser
 930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
 980 985 990

Leu Phe Trp Pro His Gln Pro Asn Gly Gln Gly Ser Phe Trp Ala Gln
 995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu
 1025 1030

<210> 2
 <211> 821
 <212> PRT
 <213> Rattus norvegicus

<400> 2

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn
 50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn
 65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met
 100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
 130 135 140

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
 145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro
 180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser
 260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe
 290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu
 325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala
 340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu
 355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu
 370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala
 405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr
 420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val
 435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser
 450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu
 465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
 485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala
 500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp
 515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu
 530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
 545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser
 565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val
 580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly
 595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe
 610 615 620

Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys
 625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu
 645 650 655

Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser
 660 665 670

Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn
 675 680 685

Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
 690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala
 705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn

```
<210> 3
<211> 3099
<212> DNA
<213> Rattus norvegicus
```

<400>	3
atggttctct gtcgcaggac cctgcacccc ttgtctctcc tggtagcaggc cgagtgctg	60
gctgaggctc tggccctggg tacacctgcct gccttcctac cctgtgaact gaagcctcat	120
ggcctggtag actgcaactg gctcttcctg aagtctgtgc ctcaattctc tgccgcagaa	180
ccccgttcca acatcaccag cctttccttg atcgccaacc gcatccacca cctgcacaac	240
ctcgactttg tccacctgcc caacgtgcga cagetgaacc tcaagtggaa ctgtccgccc	300
cctggcctca gcccttgca cttctcctgc cgcataacca ttgagcccaa aaccttcctg	360
gctatgcgca tgctggaaga gctgaacctg agctataacg gtatcaccac tgtgccccgc	420
ctgcccagct ccctgacgaa tctgagccta agccacacca acatcctggg actcgatgcc	480
agcagcctcg ctggcctgca cagcctgcga gttctcttca tggacgggaa ctgctactac	540
aagaacccct gcaacggggc ggtgaacctg accccggacg ccttctctggg cttgagcaac	600
ctcaccactc tgtcccttaa gtataacaac ctcacagagg tgccccgcca actgcccccc	660
agcctggagt acctcctgct gtcctataaac ctcatcgtca agctgggggc cgaagacctc	720
qccaacctga cctcccttcg aatgcttgat gtgggtggga attgccgtcg ctgtgatcac	780

gcccccgacc tctgtacaga atgccggcag aagtcccttg atctgcaccc tcagactttc	840
catcacctga gccaccttga aggcctggtg ctgaaggaca gttctctcca ctcgctgaac	900
tccaagtggg tccaggggtct ggcgaaacctc tcggtgctgg acctaaagcg gaactttctc	960
tacgagagca tcaacaaaac cagcgccttt cagaacctga cccgtctgcg caagctcgac	1020
ctgtccttca attactgcaa gaaggatatcg ttcgcccggc tccacctggc aagttccttc	1080
aagagcctgg tgtcgctgca ggagctgaac atgaacggca tcttcttccg cttactcaac	1140
aagaaacacgc tcaggtggct ggctgggtctg cccaagctcc acacgctgca ccttcaaattg	1200
aatttcatca accaggcgca gctcagcgtc tttagtacct tccgagccct tcgctttgtg	1260
gacctgtcca ataatcgcat cagcgggcct ccaacgctgt ccagagtcgc ccccgaaaag	1320
gcagacgagg cggagaaggg gggtccatgg cctgcaagtc tcaccccagc tctcccgagc	1380
actcccgctc caaagaactt catggtcagg tgtaagaacc tcagattcac catggacctg	1440
tctcggaaaca accaggtgac tatcaagcca gagatgttcg tcaacctctc ccatctccag	1500
tgtctgagcc tgagccacaa ctgcatcgcg caggctgtca atggctctca gttcctgccg	1560
ctgaccaacc tgaaggtgct ggacctgtcc tataacaagc tggacctgta ccattcgaaa	1620
tcgttcagtg agctcccaca gttgcaggcc ctggacctga gctacaacag ccagccattc	1680
agcatgcagg ggataggcca caacttcagt tttctggcca atctgtccag gttacagaac	1740
cttagcctgg cacacaatga cattcacagc cgcgtgtcct cagcctcta cagcacctca	1800
gtggagtatc tggacttcag cggcaacggg gtggggccgca tgtgggacga ggaggacctt	1860
tacctctatt tcttccaaga cctgagaagc ctgattcatc tggacctgtc tcagaataag	1920
ctgcacatcc tccggcccca gaacctcaac tacctcccca agagcctgac gaagctgagt	1980
ttccgtgaca atcacctctc tttctttaac tggagcagtc tggccttcct gcccaatctg	2040
cgagacctgg acctggcagg caatctacta aaggccctga ccaacggcac cctgcctaatt	2100
ggcacgctcc tccagaaact ggatgtcagt agcaacagta tcgtctttgt ggtcccagcc	2160
ttctttgctc tggcggtaga gctaaaagag gtcaacctca gccataacat cctcaagact	2220
gtggatcgct cctgggttgg gccattgtg atgaacctga cggttctaga cgtgagcagc	2280
aacctctgc attgtgcctg cggcgcaccc tttgtagact tactgctgga agtgcagacc	2340
aagggtgcctg gcctggctaa cgggtgtgaag tgtggcagtc cccgccagct gcagggccgc	2400
agcatctttg cgcaagacct gcggctgtgc ctggatgacg tcctttctcg ggactgcttt	2460
ggcctttcac tcctggctgt ggccgtgggc acgggtgttc ctttactgca gcactctgc	2520
ggctgggacg tctgggtactg tttccatctg tgccctggcat ggctaccttt gctgaccctg	2580

ggccggcgca gcgccaagc tctcccttat gatgccttcg tgggtgtcga taaggcgag 2640
 agcgcggttg ctgactgggt gtataacgag cttcgagtgc ggctagagga gcggcgcggt 2700
 cgccgagccc tacgcttggt tctggaggac cgagattggc tgcctggcca gacactcttc 2760
 gagaacctct gggcctccat ctatggcagc cgcaagactc tgtttgtgct ggccacacg 2820
 gacaaggta gtggcctcct gcgcaccagc ttcctgctgg ctgagcagcg cctgctggag 2880
 gaccgcaagg acgtgggtgt gttggtgatc ctgcgcctg atgcccaccg ctcccgctac 2940
 gtgcgactgc gccagcgcct ctgccgccag agtgtgctct tctggcccca tcagcccaac 3000
 gggcagggca gcttctgggc ccagctgagt acagccctga ctagggacaa ccaccacttc 3060
 tataaccgga acttctgccg gggacctaca gcagaatag 3099

<210> 4

<211> 2463

<212> DNA

<213> Rattus norvegicus

<400> 4

atggttctct gtcgcaggac cctgcacccc ttgtctctcc tggtagaggc cgcagtgtg 60
 gctgaggctc tggccctggg taccctgcct gccttcctac cctgtgaact gaagcctcat 120
 ggcttggttag actgcaactg gctcttcctg aagtctgtgc ctactttctc tgccgcagaa 180
 ccccgttcca acatcaccag cctttccttg atcgccaacc gcatccacca cctgcacaac 240
 ctgcactttg tccacctgcc caacgtgcga cagctgaacc tcaagtggaa ctgtccgccc 300
 cctggcctca gccccttgca cttctcctgc cgcctgacca ttgagcccaa aaccttcctg 360
 gctatgcgca tgctggaaga gctgaacctg agctataacg gtatcaccac tgtgccccgc 420
 ctgcccagct ccctgacgaa tctgagccta agccacacca acatcctggt actcgatgcc 480
 agcagcctcg ctggcctgca cagcctgcga gttctcttca tggacgggaa ctgctactac 540
 aagaacccct gcaacggggc ggtgaacgtg accccggacg ccttcctggg cttgagcaac 600
 ctacccactc tgtcccttaa gtataacaac ctacagagg tgccccgcca actgcccccc 660
 agcctggagt acctcctgct gtcctataac ctcatcgtca agctgggggc cgaagacctc 720
 gccaacctga cctcccttcg aatgcttgat gtgggtggga attgccgtcg ctgtgatcac 780
 gccccgacc tctgtacaga atgccggcag aagtccttg atctgcacc tcagactttc 840
 catcacctga gccacctga aggcctgggt ctgaaggaca gttctctcca ctgctgaac 900
 tccaagtggc tccagggctc ggcgaaacctc tcgggtgctg acctaagcga gaactttctc 960
 tacgagagca tcaacaaaac cagcgccttt cagaacctga cccgtctgcg caagctcgac 1020

```

ctgtccttca attactgcaa gaaggtatcg ttgccccgcc tccacctggc aagttccttc 1080
aagagcctgg tgtcgctgca ggagctgaac atgaacggca tcttcttccg cttactcaac 1140
aagaacacgc tcaggtggct ggctggtctg cccaagctcc acacgctgca ccttcaaattg 1200
aatttcatca accaggcgca gctcagcgtc tttagtacct tccgagccct tcgctttgtg 1260
gacctgtcca ataatcgcat cagcgggcct ccaacgctgt ccagagtcgc ccccgaaaag 1320
gcagacgagg cggagaaggg ggttccatgg cctgcaagtc tcaccccgagc tctcccgagc 1380
actcccgctc caaagaactt catggtcagg tgtaagaacc tcagattcac catggacctg 1440
tctcggaaca accaggtgac tatcaagcca gagatgttcg tcaacctctc ccatctccag 1500
tgtctgagcc tgagccacaa ctgcatcgcg caggctgtca atggctctca gttcctgccg 1560
ctgaccaacc tgaaggtgct ggacctgtcc tataacaagc tggacctgta ccattcgaaa 1620
tcgttcagtg agctcccaca gttgcaggcc ctggacctga gctacaacag ccagccattc 1680
agcatgcagg ggataggcca caacttcagt tttctggcca atctgtccag gttacagaac 1740
cttagcctgg cacacaatga cattcacagc cgcgtgtcct cagcctcta cagcacctca 1800
gtggagtatc tggacttcag cggcaacggt gtgggcccga tgtgggacga ggaggacctt 1860
tacctctatt tcttccaaga cctgagaagc ctgattcatc tggacctgtc tcagaataag 1920
ctgcacatcc tccggcccca gaacctcaac tacctcccca agagcctgac gaagctgagt 1980
ttcctgaca atcaacctctc tttctttaac tggagcagtc tggccttctc gcccaatctg 2040
cgagacctgg acctggcagg caatctacta aaggccctga ccaacggcac cctgcctaatt 2100
ggcacgctcc tccagaaact ggatgtcagt agcaacagta tcgtctttgt ggtcccagcc 2160
ttctttgctc tggcggtaga gctaaaagag gtcaacctca gccataacat cctcaagact 2220
gtggatcgct cctggtttgg gccattgtg atgaacctga cggttctaga cgtgagcagc 2280
aaccctctgc attgtgcctg cgggtgcaccc tttgtagact tactgctgga agtgcagacc 2340
aagggtgcctg gcctggctaa cgggtgtgaag tgtggcagtc cccgccagct gcagggccgc 2400
agcatctttg cgcaagacct gcggctgtgc ctggatgacg tcctttctcg ggactgcttt 2460
ggc 2463

```

```

<210> 5
<211> 1030
<212> PRT
<213> Sus scrofa

<400> 5

```

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val
 1 5 10 15

Thr Ala Leu Ala Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val
 50 55 60

Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser
 65 70 75 80

Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr
 100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
 115 120 125

Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu
 130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr
 145 150 155 160

His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn
 165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
 195 200 205

Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro
 260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg
 290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
 305 310 315 320

Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg
 325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
 340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln
 370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu
 405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
 420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro
 435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp
 450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg
 465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg
 485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn
 500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser
 515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro
 530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met
 545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu
 565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln
 580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp
 595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln
 610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His
 625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His
 645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu
 660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu
 675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg
 690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe

705		710		715		720
Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu						
	725			730		735
Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys						
	740			745		750
Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr						
	755			760		765
Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro						
	770			775		780
Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile						
	785			790		800
Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn						
	805			810		815
Cys Phe Gly Ile Ser Leu Leu Ala Met Ala Leu Gly Leu Val Val Pro						
	820			825		830
Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu						
	835			840		845
Cys Leu Ala Trp Leu Pro His Arg Gly Gln Arg Arg Gly Ala Asp Ala						
	850			855		860
Leu Phe Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val						
	865			870		875
Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg						
	885			890		895
Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro						
	900			905		910
Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg						
	915			920		925
Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu						
	930			935		940

Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys
 945 950 955 960

Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala Tyr Arg Ser Arg
 965 970 975

Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp
 980 985 990

Pro His Gln Pro Arg Gly Gln Gly Ser Phe Trp Ala Gln Leu Gly Thr
 995 1000 1005

Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg Asn Phe Cys
 1010 1015 1020

Arg Gly Pro Thr Thr Ala Glu
 1025 1030

<210> 6
 <211> 819
 <212> PRT
 <213> Sus scrofa

<400> 6

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val
 1 5 10 15

Thr Ala Leu Ala Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val
 50 55 60

Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser
 65 70 75 80

Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr
 100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
 115 120 125

Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu
 130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr
 145 150 155 160

His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn
 165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
 195 200 205

Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro
 260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg
 290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
 305 310 315 320

Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg
 325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
 340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln
 370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu
 405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
 420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro
 435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp
 450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg
 465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg
 485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn
 500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser
 515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro
 530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met
 545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu
 565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln
 580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp
 595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln
 610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His
 625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His
 645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu
 660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu
 675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg
 690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe
 705 710 715 720

Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu
 725 730 735

Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys
 740 745 750

Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr
 755 760 765

Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro
 770 775 780

Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile
 785 790 795 800

Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn
 805 810 815

Cys Phe Gly

<210> 7
 <211> 3352
 <212> DNA
 <213> Sus scrofa

<400> 7
 gagcacgaac atccttcact gtagctgctg cccggtctgc cagccagacc ctttgagaa 60
 gacccactc cctgtcatgg gccccgctg caccctgcac cccctttctc tcctgggtgca 120
 ggtgacagcg ctggctgcgg ctctggccca gggcaggctg cctgccttcc tgccctgtga 180
 gctccagccc caccggcctgg tgaactgcaa ctggctcttc ctgaagtccg tgccccactt 240
 ctggcgaggca ggcggcgagg ccaacgtcac cagcctctcc ttactctcca accgcatcca 300
 ccacctgcac gactccgact tcgtccacct gtccagccta cgaactctca acctcaagtg 360
 gaactgcccc cgggctggcc tcagcccat gcacttcccc tgccacatga ccacgagcc 420
 caacaccttc ctggcctgct ccacctgga ggagctgaac ctgagctaca acagcatcac 480
 gaccgtgcct gccctgcccg actccctcgt gtccctgtcg ctgagccgca ccaacatcct 540
 ggtgctagac cccacccacc tcaactggcct acatgccctg cgctacctgt acatggatgg 600
 caactgctac tacaagaacc cctgccaggg ggcgctggag gtggtgccgg gtgccctcct 660
 cggcctgggc aacctcacac atctctcact caagtacaac aatctcacgg aggtgccccg 720
 cagcctgccc cccagcctgg agacctgct gttgtcctac aaccacattg tcacctgac 780
 gcctgaggac ctggccaatc tgactgccct gcgcgtgctt gatgtggggg ggaactgccg 840
 ccgctgtgac catgccccga acccctgcag ggagtgccca aaggaccacc ccaagctgca 900
 ctctgacacc ttcagccacc tgagccgct cgaaggcctg gtgttgaaag acagttctct 960
 ctacaacctg gacaccaggt ggttcgagg cctggacagg ctccaagtgc tggacctgag 1020
 tgagaacttc ctctacgact gcatcaccaa gaccacggcc ttccagggcc tggcccgact 1080
 ggcgagcctc aacctgtcct tcaattacca caagaaggctg tcctttgcc acctgacact 1140
 ggcacctcc tttgggcacc tcgggtccct gaaggagctg gacatgcatg gcattctctt 1200
 ccgctcgctc agtgagacca cgctccaacc tctgggtcaa ctgcctatgc tccagacct 1260
 gcgctgcag atgaacttca ttaaccaggc ccagctcagc atctttgggg ccttccttgg 1320
 cctgctgtac gtggacctat cggacaaccg catcagcga gctgcaaggc cagtggccat 1380
 tactagggag gtggatggtg gggagagggt ctggctgcct tccaggaacc tcgctccacg 1440
 tccactggac actctccgct cagaggactt catgccaac tgcaaggcct tcagcttcac 1500

cttgacctg tctcggaaca acctggtgac aatccagtcg gagatgtttg ctgcctctc	1560
acgcctcgag tgctgcgcc tgagccacaa cagcatctcc caggcgggtca atggctctca	1620
gtttgtgccg ctgaccagcc tgcgggtgct ggacctgtcc cacaacaagc tggacctgta	1680
tcacgggagc tcgttcacgg agctgccgag cctggaagca ctggacctca gctacaatag	1740
ccagcccttt accatgcagg gtgtgggcca caacctcagc ttcgtggccc agctgcccgc	1800
cctgcgctac ctgacctgg cgacacatga catccatagc cgagtgtccc agcagctctg	1860
tagcgctca ctgtgcccc tggacttttag cggcaacgat ctgagccgga tgtgggctga	1920
gggagacctc tatctccgct tcttccaagg cctaagaagc ctagtctggc tggacctgtc	1980
ccagaaccac ctgcacaccc tcctgccagc tgccctggac aacctcccca aaagcctgaa	2040
gcatctgcat ctccgtgaca ataacctggc cttcttcaac tggagcagcc tgacctctct	2100
gccaagctg gaaaccttg acttggtgg aaaccagctg aaggccctaa gcaatggcag	2160
cctgccatct ggcacccagc tgcggaggct ggacctcagt ggcaacagca tcggctttgt	2220
gaacctggc tcttttgccc tggccaagca gttagaagag ctcaacctca gcgccaatgc	2280
cctcaagaca gtggagccct cctggtttgg ctgatggtg ggcaacctga aagtcctaga	2340
cgtgagcgcc aacctctgc actgtgcctg tggggcgacc ttcgtgggct tcctgctgga	2400
ggtagaggct gccgtgcctg ggctgccag ccgctcaag tgtggcagtc cggggcagct	2460
ccagggccat agcatctttg cgcaagacct gcgctctgc ctggatgaga ccctctcgtg	2520
gaactgtttt ggcatctgc tgcaggccat ggccctgggc ctggttgtgc ccatgctgca	2580
ccacctctgc ggctgggacc tctggtactg cttccacctg tgccctggcct ggctgcccc	2640
ccgagggcag cggcggggag cagacgccct gttctatgat gccttcgtgg tctttgacaa	2700
agctcagagt gctgtggccg actgggtgta caacgagctg cgggtgcagc tggaggagcg	2760
ccgtgggagc cgcgcactgc gcctgtgcct ggaggagcga gactgggttac ctggcaagac	2820
gctcttcgag aacctgtggg cctcagtcta cagcagccgc aagacctgt ttgtgctggc	2880
ccacacggac cgtgtcagcg gcctcttgag tgccagtttc ctgctggccc agcagcgct	2940
gctggaggac cgcaaggacg ttgtagtgtt ggtgatcctg cgcgccgatg cctaccgctc	3000
ccgtacgtg cggctgcgcc agcgctctg ccgccagagt gtctctctct gggccaccca	3060
gccccgtggg cagggcagct tctgggcccc gctgggcaca gccctgacca gggacaacca	3120
ccacttctat aaccggaact tctgcggggg cccacgaca gccgaatagc actgagtgc	3180
agccagttg cccagcccc cctggatttg cctctctgcc tggggtgccc caacctgctt	3240
tgctcagcca caccactgct ctgctccctg tccccaccc cccccccag cctggcatgt	3300

aacatgtgcc caataaatgc taccggaggg ccaagaaaaa aaaaaaaaaa aa 3352

<210> 8
 <211> 2457
 <212> DNA
 <213> Sus scrofa

<400> 8
 atgggcccc gctgcaccct gcaccccctt tctctcctgg tgcaggtgac agcgtggt 60
 gcggctctgg ccagggcag gctgcctgcc ttctgacct gtgagctcca gcccacggc 120
 ctggtgaact gcaactggct cttcctgaag tccgtgcccc acttctcggc ggcagcgccc 180
 cgggccaacg tcaccagcct ctccttactc tccaaccgca tccaccacct gcacgactcc 240
 gacttcgtcc acctgtccag cctacgaact ctcaacctca agtggaaactg cccgccggct 300
 ggcctcagcc ccattgcactt cccctgccac atgacctcg agcccaacac cttcctggcc 360
 gtgcccaccc tggaggagct gaacctgagc tacaacagca tcacgacctg gcctgccctg 420
 cccgactccc tcgtgtccct gtcgctgagc cgcaccaaca tcctggtgct agacccacc 480
 cacctcactg gcctacatgc cctgcgtac ctgtacatgg atggcaactg ctactacaag 540
 aaccctgcc agggggcgct ggaggtggtg ccgggtgccc tcctcggcct gggcaacctc 600
 acacatctct cactcaagta caacaatctc acggaggtgc cccgcagcct gcccccagc 660
 ctggagaccc tgctgttgtc ctacaaccac attgtcacc tgacgcctga ggacctggcc 720
 aatctgactg ccctgcgcgt gcttgatgtg ggggggaact gccgccgctg tgacctgcc 780
 cgcaaccct gcagggagtg ccaaaggac caccacaagc tgcactctga caccttcagc 840
 cacctgagcc gcctcgaagg cctggtgttg aaagacagtt ctctctaaa cctggacacc 900
 aggtggttcc gaggcctgga caggctccaa gtgctggacc tgagtgagaa cttcctctac 960
 gactgcatca ccaagaccac ggccttccag ggcctggccc gactgcgcag cctcaacctg 1020
 tccttcaatt accacaagaa ggtgtccttt gccacctgc acctggcacc ctcctttggg 1080
 cacctccggt ccctgaagga gctggacatg catggcatct tcttcgctc gctcagttag 1140
 accacgtccc aacctctggt ccaactgcct atgctccaga ccctgcgcct gcagatgaac 1200
 ttcattaacc agggccagct cagcatcttt ggggccttec ctggcctgct gtacgtggac 1260
 ctatcggaca accgcatcag cggagctgca aggccagtgg ccattactag ggaggtgat 1320
 ggtagggaga gggctctggct gccttccagg aacctcgctc caagtccact ggacactctc 1380
 cgctcagagg acttcatgcc aaactgcaag gccttcagct tcaccttga cctgtctcgg 1440
 aacaacctgg tgacaatcca gtcggagatg tttgctcgcc tctcacgcct cgagtgcctg 1500

cgctgagcc acaacagcat ctcccaggcg gtcaatggct ctgagtttgt gccgctgacc 1560
 agcctgcggg tgctggacct gtcccacaac aagctggacc tgtatcacgg gcgctcgttc 1620
 acggagctgc cgcgcctgga agcactggac ctgagctaca atagccagcc ctttaccatg 1680
 caggggtgtgg gccacaacct cagcttcgtg gccagctgc ccgccctgcg ctacctcagc 1740
 ctggcgacaca atgacatcca tagccgagtg tcccagcagc tctgtagcgc ctactgtgc 1800
 gccctggact ttagcggcaa cgatctgagc cggatgtggg ctgagggaga cctctatctc 1860
 cgcttcttcc aaggcctaag aagcctagtc tggctggacc tgtcccagaa ccacctgcac 1920
 accctcctgc cacgtgccct ggacaacctc cccaaaagcc tgaagcatct gcatctccgt 1980
 gacaataacc tggccttctt caactggagc agcctgacct tcctgcccga gctggaaacc 2040
 ctggacttgg ctggaaacca gctgaaggcc ctaagcaatg gcagcctgcc atctggcacc 2100
 cagctgcgga ggctggacct cagtggcaac agcatcggct ttgtgaacct tggcttcttt 2160
 gccctggcca agcagttaga agagctcaac ctgagcgcca atgccctcaa gacagtggag 2220
 cctccttggt ttggctcgat ggtgggcaac ctgaaagtcc tagacgtgag cgccaaccct 2280
 ctgcactgtg cctgtggggc gaccttcgtg ggcttcctgc tggaggtaca ggctgccgtg 2340
 cctgggctgc ccagccgct caagtgtggc agtccggggc agtccaggg ccatagcatc 2400
 ttgcgcaag acctgcgcct ctgcctggat gagaccctct cgtggaactg ttttggc 2457

<210> 9
 <211> 1029
 <212> PRT
 <213> Bos taurus

<400> 9

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
 1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
 50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
 65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr

305		310		315		320
Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg	325		330		335	
Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His	340		345		350	
Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu	355		360		365	
Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln	370		375		380	
Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn	385		390		395	400
Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu	405		410		415	
Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro	420		425		430	
Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu	435		440		445	
Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp	450		455		460	
Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn	465		470		475	480
Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu	485		490		495	
Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly	500		505		510	
Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His	515		520		525	
Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln	530		535		540	

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
 660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val
 705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
 725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
 755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
805 810 815

Phe Gly Leu Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met
820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys
835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu
850 855 860

Leu Tyr Asp Ala Val Val Val Phe Asp Lys Val Gln Ser Ala Val Ala
865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly
885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly
900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys
915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg
930 935 940

Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp
945 950 955 960

Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr
965 970 975

Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro
980 985 990

His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Ile Ala
995 1000 1005

Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg
1010 1015 1020

Gly Pro Thr Thr Ala Glu
1025

<210> 10
<211> 818
<212> PRT
<213> Bos taurus

<400> 10

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu
20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe
35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
 195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
 260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
 290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
 305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg
 325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
 340 345 350

Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln
 370 375 380

Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro

420	425	430
Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu		
435	440	445
Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp		
450	455	460
Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn		
465	470	475
Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu		
485	490	495
Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly		
500	505	510
Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His		
515	520	525
Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln		
530	535	540
Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln		
545	550	555
Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg		
565	570	575
Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys		
580	585	590
Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu		
595	600	605
Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly		
610	615	620
Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr		
625	630	635
Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu		
645	650	655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
 660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val
 705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
 725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
 755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
 785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
 805 810 815

Phe Gly

<210> 11

<211> 3191

<212> DNA

<213> Bos taurus

<400> 11

gggaagtggg cgccaagcat ccttccctgc agctgcctcc caacctgccc gccagaccct	60
ctggagaagc cgcattccct gtcattggcc cctactgtgc cccgcacccc ctttctctcc	120
tgggtgcaggc ggcggcactg gcagcggccc tggccgaggg caccctgcct gccttctctgc	180
cctgtgagct ccagcccat ggtcaggtgg actgcaactg gctgttctctg aagtctgtgc	240
cgcacttttc ggctggagcc ccccgggcca atgtcaccag cctctctcta atctccaacc	300

gcatccacca cttgcatgac tctgacttcg tccacctgtc caacctgcgg gtcctcaacc 360
 tcaagtggaa ctgcccgcg gccggcctca gcccctgca cttcccctgc cgtatgacca 420
 tcgagcccaa caccttctcg gctgtgcca ccctggagga gctgaacctg agctacaacg 480
 gcatcacgac cgtgcctgcc ctgcccagtt ccctcgtgtc cctgtcgtg agccacacca 540
 gcatcctggg gctaggcccc acccacttca ccggcctgca cggcctgcgc tttctgtaca 600
 tggacggcaa ctgctactac atgaaccctt gccgcgggc cctggagggtg gcccagggc 660
 ccctcctcgg cctgggcaac ctcacgcacc tgtcgtcaa gtacaacaac ctcacggagg 720
 tgccccgcg cctgcccccc agcctggaca ccctgctgt gtcctacaac cacattgtca 780
 ccctggcacc cgaggacctg gccaacctga ctgccctgcg cgtgcttgac gtgggtggga 840
 actgccgcg ctgcgaccat gcccgcaacc cctgcaggga gtgcccagg aacttcccc 900
 agctgcaccc tgacaccttc agtcacctga gccgcctcga aggcctgggt ttgaaggaca 960
 gttctctcta caaactagag aaagattggg tccgcggcct gggcaggctc caagtgtcg 1020
 acctgagtga gaacttcctc tatgactaca tcaccaagac caccatcttc aacgacctga 1080
 ccagctgcg cagactcaac ctgtccttca attaccacaa gaagggtgcc ttcgcccacc 1140
 tgcacctagc gtcctccttt gggagtctgg tgtccctgga gaagctggac atgcacggca 1200
 tcttcttcg ctccctcacc aacatcacgc tccagtgcgt gaccggctg cccaagctcc 1260
 agagtctgca tctgcagctg aacttcacat accaggccca gctcagcatc tttggggcct 1320
 tcccagcct gctcttcgtg gacctgtcgg acaaccgcat cagcggagcc gcgacgccag 1380
 cggccgccct gggggagggtg gacagcaggg tggaagtctg gcgattgccc aggggcctcg 1440
 ctccaggccc gctggacgcc gtcagctcaa aggacttcat gccaaagtgc aacctcaact 1500
 tcaccttggg cctgtcacgg aacaacctgg tgacaatcca gcaagagatg tttaccgcc 1560
 tctccgcct ccagtgcctg cgctgagcc acaacagcat ctcgcaggcg gttaatggct 1620
 ccagttcgt gccgctgacc agcctgcgag tgctcgacct gtcccacaac aagctggacc 1680
 tgtaccatgg gcgctcattc acggagctgc cgcagctgga ggcactggac ctcagctaca 1740
 acagccagcc cttcagcatg cagggcgtgg gccacaacct cagcttcgtg gccagctgc 1800
 cctccctgcg ctacctcagc cttgcgcaca atggcatcca cagccgcgtg tcacagaagc 1860
 tcagcagcgc ctcgttgccg gccctggact tcagcggcaa ctccctgagc cagatgtggg 1920
 ccgagggaga cctctatctc tgctttttca aaggcttgag gaacctggtc cagctggacc 1980
 tgtccgagaa ccatctgcac accctcctgc ctcgtcacct ggacaacctg cccaagagcc 2040

tgcggcagct gcgtctccgg gacaataacc tggccttctt caactggagc agcctgaccg 2100
 tcctgccccg gctggaagcc ctggatctgg caggaaacca gctgaaggcc ctgagcaacg 2160
 gcagcctgcc gcctggcatc cggctccaga agctggacgt gagcagcaac agcatcggct 2220
 tcgtgatccc cggcttcttc gtccgcgcga ctccggctgat agagcttaac ctcagcgcca 2280
 atgccctgaa gacagtggat ccctcctggg tcggttcctt agcagggacc ctgaaaatcc 2340
 tagacgtgag cgccaaccgg ctccactgcg cctgcggggc ggcctttgtg gacttcctgc 2400
 tggagagaca ggaggccgtg cccgggctgt ccaggcgcgt cacatgtggc agtccgggcc 2460
 agctccaggg ccgcagcatc ttcacacagg acctgcgcct ctgcctggat gagaccctct 2520
 ccttggaactg ctttggcctc tcaactgctaa tgggtggcgt gggcctggca gtgcccatgc 2580
 tgcaccacct ctgtggctgg gacctctggg actgcttcca cctgtgtctg gccatttgc 2640
 cccgacggcg gcggcagcgg ggcgaggaca cctgctcta tgatgccgtc gtggtcttcg 2700
 acaaggtgca gagtgcagtg gctgattggg tgtacaacga gctccgcgtg cagctggagg 2760
 agcgccgggg gcgccggggc ctccgcctct gcctggagga gcgagactgg ctccctggta 2820
 agacgctctt cgagaacctg tgggcctcgg tctacagcag ccgcaagacc atgttcgtgc 2880
 tggaccacac ggaccgggtc agcggcctcc tgcgcgccag ctctctgctg gccagcagc 2940
 gcctgttggg ggaccgcaag gacgtcgtag tgctgggtgat cctgcgcccc gccgcctatc 3000
 ggtcccgtc cgtgcggctg cgcagcgcc tctgccgcca gacgctcctc ctctggcccc 3060
 accagcccag tggccagggt agtttctggg ccaacctggg catagccctg accagggaca 3120
 accgtcactt ctataaccgg aacttctgcc ggggccccac gacagccgaa tagcacagag 3180
 tgactgccc g 3191

<210> 12

<211> 2454

<212> DNA

<213> Bos taurus

<400> 12

atgggcccct actgtgcccc gcaccccctt tctctcctgg tgcaggcggc ggcactggca 60
 gcggccctgg ccgagggcac cctgcctgcc ttctgcct gtgagctcca gcccattgg 120
 caggtggact gcaactggct gttcctgaag tctgtgccgc acttttcggc tggagcccc 180
 cgggccaatg tcaccagcct ctcttaatc tccaaccgca tccaccactt gcatgactct 240
 gacttcgtcc acctgtccaa cctgcgggtc ctcaacctca agtggaaactg cccgcgggcc 300
 ggctcagcc ccatgcactt cccctgcgt atgacatcg agcccaaac cttcctggct 360

gtgcccaccc tggaggagct gaacctgagc tacaacggca tcacgaccgt gcctgccttg	420
cccagttccc tcgtgtccct gtcgtgagc cacaccagca tcctgggtgct aggccccacc	480
cacttcaccg gcctgcacgc cctgcgcttt ctgtacatgg acggcaactg ctactacatg	540
aacctctgcc cgcggggccct ggagggtggc ccaggcgccc tcctcggcct gggcaacctc	600
acgcacctgt cgctcaagta caacaacctc acggagggtgc cccgcgcct gccccccagc	660
ctggacaccc tgctgctgtc ctacaaccac attgtcacc tggcaccga ggacctggcc	720
aacctgactg ccctgcgcgt gcttgacgtg ggtgggaact gccgcgcgt cgacctgccc	780
cgcaaccct gcagggagtg cccaaagaac ttccccaagc tgcacctga caccttcagt	840
cacctgagcc gcctcgaagg cctggtgttg aaggacagtt ctctctacaa actagagaaa	900
gattggttcc gcggcctggg caggtccaa gtgctcgacc tgagtgagaa ctctctctat	960
gactacatca ccaagaccac catcttcaac gacctgacct agctgcgcag actcaacctg	1020
tccttcaatt accacaagaa ggtgtccttc gccacctgc acctagcgtc ctcttttggg	1080
agtctggtgt ccctggagaa gctggacatg cacggcatct tcttcgcctc cctcaccaac	1140
atcacgctcc agtcgctgac ccggctgccc aagctccaga gtctgcatct gcagctgaac	1200
ttcatcaacc aggccagct cagcatcttt ggggccttcc cgagcctgct ctctgtggac	1260
ctgtcggaca accgcatcag cggagccgcg acgccagcgg ccgccctggg ggagggtggac	1320
agcaggggtg aagtctggcg attgccagg ggcctcgctc caggcccgct ggacgccgtc	1380
agctcaaagg acttcatgcc aagctgcaac ctcaacttca ccttggaact gtcacggaac	1440
aacctggtga caatccagca agagatgttt accgcctct cccgcctcca gtgcctgcgc	1500
ctgagccaca acagcatctc gcaggcgggt aatggctccc agttcgtgcc gctgaccagc	1560
ctgcgagtgc tcgacctgtc ccacaacaag ctggacctgt accatgggcg ctcattcacg	1620
gagctgccgc agctggaggc actggacctc agctacaaca gccagccctt cagcatgcag	1680
ggcgtgggccc acaacctcag ctctgtggcc cagctgcct ccctgcgcta cctcagcctt	1740
gcgcacaatg gcatccacag ccgcgtgtca cagaagctca gcagcgcctc gttgcgcgcc	1800
ctggacttca gcggcaactc cctgagccag atgtgggccc agggagacct ctatctctgc	1860
tttttcaaag gcttgaggaa cctggtccag ctggacctgt ccgagaacca tctgcacacc	1920
ctcctgcctc gtcacctgga caacctgccc aagagcctgc ggagctgcg tctccgggac	1980
aataacctgg ccttcttcaa ctggagcagc ctgacctcc tgcgccggt ggaagccctg	2040
gatctggcag gaaaccagct gaaggccctg agcaacggca gcctgccgcc tggcatccgg	2100
ctccagaagc tggacgtgag cagcaacagc atcggtctcg tgatccccgg cttcttcgtc	2160

cgcgcgactc ggctgataga gcttaacctc agcgccaatg ccctgaagac agtggatccc 2220
 tcctggttcg gttccttagc agggaccctg aaaatcctag acgtgagcgc caaccgcgc 2280
 cactgcgcct gcggggcggc ctttgtggac ttctgtctgg agagacagga ggccgtgccc 2340
 gggctgtcca ggcgcgtcac atgtggcagt ccgggccagc tccagggccg cagcatcttc 2400
 acacaggacc tgcgcctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 13
 <211> 1031
 <212> PRT
 <213> Equus caballus

<400> 13

Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn
 50 55 60

Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp
 65 70 75 80

Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met
 100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
 130 135 140

Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro
 145 150 155 160

Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe
 260 265 270

Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe
 290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
 340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu
 370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly
 405 410 415
 Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu
 420 425 430
 Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu
 435 440 445
 Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu
 450 455 460
 Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser
 465 470 475 480
 Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser
 485 490 495
 Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val
 500 505 510
 Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
 515 520 525
 Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
 530 535 540
 Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
 545 550 555 560
 Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr
 565 570 575
 Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser
 580 585 590
 Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn
 595 600 605
 Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe
 610 615 620
 Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu
 625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln
 645 650 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
 660 665 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln
 675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln
 690 695 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe
 705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
 725 730 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu
 740 745 750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
 755 760 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp
 805 810 815

Asp Cys Phe Gly Leu Ser Leu Leu Val Val Ala Leu Gly Leu Ala Met
 820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His
 835 840 845

Leu Gly Leu Ala Trp Leu Pro Arg Arg Gly Trp Gln Arg Gly Ala Asp
 850 855 860

Ala Leu Ser Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala

865 870 875 880
 Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg
 885 890 895
 Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu
 900 905 910
 Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser
 915 920 925
 Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Gln Val Ser Gly Leu
 930 935 940
 Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg
 945 950 955 960
 Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Ala Arg Arg Ser
 965 970 975
 Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Phe
 980 985 990
 Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly
 995 1000 1005
 Met Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln Asn Phe
 1010 1015 1020
 Cys Arg Gly Pro Thr Met Ala Glu
 1025 1030

 <210> 14
 <211> 820
 <212> PRT
 <213> Equus caballus

 <400> 14
 Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln
 1 5 10 15
 Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe
 20 25 30
 Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu

35	40	45
Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn		
50	55	60
Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp		
65	70	75 80
Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp		
	85	90 95
Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met		
	100	105 110
Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu		
	115	120 125
Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser		
	130	135 140
Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro		
	145	150 155 160
Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly		
	165	170 175
Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro		
	180	185 190
Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr		
	195	200 205
Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr		
	210	215 220
Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu		
	225	230 235 240
Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg		
	245	250 255
Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe		
	260	265 270

Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe
 290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
 340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu
 370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly
 405 410 415

Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu
 420 425 430

Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu
 435 440 445

Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu
 450 455 460

Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser
 465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser
 485 490 495

Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val
 500 505 510

Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
 515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
 530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
 545 550 555 560

Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr
 565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser
 580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn
 595 600 605

Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe
 610 615 620

Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu
 625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln
 645 650 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
 660 665 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln
 675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln
 690 695 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe
 705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
 725 730 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu
 740 745 750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
 755 760 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp
 805 810 815

Asp Cys Phe Gly
 820

<210> 15
 <211> 3391
 <212> DNA
 <213> Equus caballus

<400> 15
 ctctgttctc tgagctgttg ccgctgaag ggactgag cacaagcat cctcctctgc 60
 agctgctgcc cagtgtgcca gctggacct ctggatcatc tccactccc tgcatgggc 120
 ccttgccatg gtgccctgca gccctgtct ctctggtgc aggcggccat gctggcctg 180
 gctctggccc aaggcacct gcctcccttc ctgccctgtg agctccagcc ccacggcctg 240
 gtgaactgca actggctgtt cctgaagtcc gtgccccact tctcagcagc agcaccctgg 300
 gacaatgtca ccagcctttc cttgtctctc aaccgcatcc accacctcca cgactccgac 360
 tttgccaac tgtccaacct gcagaaactc aacctcaaat ggaactgccc gccagccggc 420
 ctgagcccca tgcacttccc ctgccacatg accatcgagc ccaacacttt cctggctgta 480
 cccaccctgg aggagctgaa cctgagctac aacggcatca cgactgtgcc tgccctgccc 540
 agctccctcg tgtccctgat cctgagccgc accaacatcc tgcagctaga cccaccagc 600
 ctcacgggcc tgcattgccct gcgcttcccta tacatggatg gcaactgcta ctacaagaac 660
 ccctgcgggc gggccctgga ggtggcccca ggcgcctcc ttggcctggg caacctcacc 720
 cacctgtcac tcaagtacaa caacctcaca acggtgcccc gcagcctgcc ccctagcctg 780
 gactacctgc tgttgccta caaccacatt gtcacctgg cacctgagga cctggccaat 840
 ctgactgccc tgcgtgtgct cgatgtgggt ggaaactgcc gccgctgtga ccatgcacgc 900
 aaccctgcg tggagtgcc acataaattc cccagctgc actccgacac cttcagccac 960

ctaagccgcc tagaaggcct cgtgttgaag gatagttctc tctaccagct gaaccccaga 1020
 tggttccgtg gcctgggcaa cctcacagtg ctgcacctga gtgagaactt cctctacgac 1080
 tgcataacca aaaccaaggc attccagggc ctggcccagc tgcgaagact caacttgtcc 1140
 ttcaattacc ataagaaggt gtccttcgcc cacctgacgc tggcaccctc cttcggggagc 1200
 ctgctctccc tgcaggaact ggacatgcat ggcatcttct tccgctcact cagccagaag 1260
 acgctccagc cactggcccc cctgcccctg ctccagcgtc tgtatctgca gatgaacttc 1320
 atcaaccagg ccagctcgg catcttcaag gacttccctg gtctgcgcta catagacctg 1380
 tcagacaacc gcatcagtgg agctgtggag ccggtggcca ccacagggga ggtggatggt 1440
 gggaagaagg tctggctgac atccaggagc ctactccag gccactgga cccccccagc 1500
 tctgaggact tcatgccaa gtgcaagaac ctacagcttca ccttggaact gtcacggaac 1560
 aacctggtaa cagtccagcc agagatgttt gccagctct cgcgcctcca gtgcctgcgc 1620
 ctgagccaca acagcatctc gcaggcggtc aatggctcac agttcgtgcc actgaccagc 1680
 ctgcagggtgc tggacctgct ccataacaaa ctggacctgt accatgggag ctcggtttacg 1740
 gagctgccgc gactggaggc cctggacctc agctacaaca gccagccctt cagcatgcgg 1800
 ggtgtggggc acaacctcag ctttgtggcc cagctgcccc cctgcgcta cctcagcctg 1860
 gcacacaatg gcatccacag ccgtgtgtcc cagcagctct gcagcacctc gctgtggggc 1920
 ctggacttca ggggcaattc cctgagccag atgtgggctg agggagacct ctatctccgc 1980
 ttcttccaag gcctgagaag cctaaccgg ctagacctgt ccagaatcg tctgcatacc 2040
 ctctgccat gcacctggg caacctcccc aagagcttgc agctgctgag tctccgtaac 2100
 aattacctgg ccttcttcaa ttggagcagc ctgacctcc tgcaccaact ggaaacctg 2160
 gacctggctg gaaaccagct gaaggctctg agcaatggca gcctgccttc tggcaccag 2220
 ctccagaggc tggacgtcag caggaacagc atcatcttcg tggccctgg cttctttgct 2280
 ctggccacga ggctgcgaga gctcaacctc agtgccaacg ccctcaggac agaggagccc 2340
 tcctggtttg gtttcctagc aggctccctt gaagtcctag atgtgagcgc caacctctg 2400
 cactgagcct gtggggcagc ctttgtggac ttctgctgc aggttcaggc tgccgtgcct 2460
 ggtctgccc a ggcgcgtcaa gtgtggcagt ccggggcagc tccagggccg cagcatcttc 2520
 gcacaagacc tgcgcctctg cctggacaag tccctctcct gggactgttt tggctcttca 2580
 ttgtggttg tggccctggg cctggccatg cctatgttgc accacctctg cggctgggac 2640
 ctctggtact gcttccacct gggcctggcc tggctgcccc ggcgggggtg gcagcggggc 2700

gcggatgccc tgagctatga tgcctttgtg gtcttcgaca aggcacagag cgcagtggcc 2760
 gactgggtgt acaatgaact gcgggtgctg ctagaggagc gccgtgggcg ccgggagctc 2820
 cgcctgtgtc tggaggagcg tgactggcta cctggcaaga cgctgttcga aaacctgtgg 2880
 gcctcagtct acagcagccg caagatgctg tttgtgctgg cccacacgga ccaggtcagt 2940
 ggcctcttgc gtgccagctt cctgctggcc cagcagcgtc tgctggagga ccgcaaggac 3000
 gttgtggtgc tggtaatcct gagccctgac gccgcgctt cccgttacgt gcggtgctgc 3060
 cagcgctctc gccgccagag tgcctcttcc tggccccacc agcctagtgg ccagcgcagc 3120
 ttctggggcc agctaggcat ggccctgacc agggacaacc gccacttcta taaccagaac 3180
 ttctgccggg gcccgacgat ggctgagtag cacagagtga cagcctggca tgtacaaccc 3240
 ccagccctga ccttgccctc ctgcctatga tgcccagtct gcctcactct gtgacgcccc 3300
 tgctctgcct ccgccaccct caccctggc atacagcagg cactcaataa atgccactgg 3360
 caggccaaac agccaaaaa aaaaaaaaaa a 3391

<210> 16

<211> 2460

<212> DNA

<213> Equus caballus

<400> 16

atgggcccctt gccatggtgc cctgcagccc ctgtctctcc tgggtgcaggc ggccatgctg 60
 gccgtggctc tggcccaagg caccctgcct cccttcctgc cctgtgagct ccagccccac 120
 ggcctggtga actgcaactg gctgttcctg aagtccgtgc cccacttctc agcagcagca 180
 ccccgggaca atgtcaccag cctttccttg ctctccaacc gcattccacca cctccacgac 240
 tccgactttg cccaactgtc caacctgcag aaactcaacc tcaaattggaa ctgcccggca 300
 gccggcctca gcccctatgca cttcccctgc cacatgacca tcgagcccaa cactttcctg 360
 gctgtaccca ccctggagga gctgaacctg agctacaacg gcattcacgac tgtgcctgcc 420
 ctgcccagct ccctcggtc cctgatcctg agccgcacca acatcctgca gctagacccc 480
 accagcctca cgggcctgca tgccctgcgc ttcctataca tggatggcaa ctgctactac 540
 aagaaccctt gcggggcggc cctggagggtg gcccagcgcc cctccttgg cctgggcaac 600
 ctcaccacc tgtcactcaa gtacaacaac ctcaaacgg tgccccgcag cctgccccct 660
 agcctggagt acctgctgtt gtctacaac cacattgtca ccctggcacc tgaggacctg 720
 gccaatctga ctgccctgcg tgtgctcgat gtgggtggaa actgccgccc ctgtgacctat 780
 gcacgcaacc cctgcgtgga gtgcccacat aaattcccc agctgcactc cgacaccttc 840

agccacctaa gccgcctaga aggcctcgtg ttgaaggata gttctctcta ccagctgaac 900
 cccagatggg tccgtggcct gggcaacctc acagtgcctg acctgagtga gaacttcctc 960
 tacgactgca tcacaaaaac caaggcattc cagggcctgg cccagctgcg aagactcaac 1020
 ttgtccttca attaccataa gaagggtgcc ttgcgccacc tgacgctggc accctccttc 1080
 gggagcctgc tctccctgca ggaactggac atgcatggca tcttcttcgg ctcactcagc 1140
 cagaagacgc tccagccact ggcccgcctg cccatgctcc agcgtctgta tctgcagatg 1200
 aacttcatca accaggccca gctcggcatc ttcaaggact tccctgggtc gcgctacata 1260
 gacctgtcag acaaccgcat cagtggagct gtggagccgg tggccaccac aggggaggtg 1320
 gatggtgagg agaaggctctg gctgacatcc agggacctca ctccaggccc actggacacc 1380
 cccagctctg aggacttcat gccaaagtgc aagaacctca gcttcacctt ggacctgtca 1440
 cggaacaacc tggtaacagt ccagccagag atgtttgcc agctctcggc cctccagtgc 1500
 ctgcgcctga gccacaacag catctcgcag gcggtcaatg gctcacagtt cgtgccactg 1560
 accagcctgc aggtgctgga cctgtcccat aacaaactgg acctgtacca tgggcgctcg 1620
 tttagcgagc tgccgcgact ggaggccctg gacctcagct acaacagcca gcccttcagc 1680
 atgcgggggtg tgggccacaa cctcagcttt gtggcccagc tgcccaccct gcgctacctc 1740
 agcctggcac acaatggcat ccacagccgt gtgtcccagc agctctgcag cacctcgtg 1800
 tgggccctgg acttcagcgg caattccctg agccagatgt gggctgaggg agacctctat 1860
 ctccgcttct tccaaggcct gagaagccta atccggctag acctgtcca gaatcgtctg 1920
 cataccctcc tgccatgcac cctgggcaac ctccccaaga gcttgagct gctgcgtctc 1980
 cgtaacaatt acctggcctt cttcaattgg agcagcctga ccctcctgcc caacctggaa 2040
 acctggacc tggctggaaa ccagctgaag gctctgagca atggcagcct gccttctggc 2100
 acccagctcc agaggctgga cgtcagcagg aacagcatca tcttcgtggc ccctggcttc 2160
 tttgctctgg ccacgaggct gcgagagctc aacctcagt ccaacgccct caggacagag 2220
 gagccctcct ggtttggttt cctagcaggc tcccttgaag tctagatgt gagcgccaac 2280
 cctctgcact gcgcctgtgg ggcagccttt gtggacttcc tgctgcaggt tcaggctgcc 2340
 gtgectggtc tgcccagccg cgtcaagtgt ggcagtccgg gccagctcca gggccgcagc 2400
 atcttcgcac aagacctgcg cctctgcctg gacaagtccc tctcctggga ctgttttggt 2460

<210> 17

<211> 1029

<212> PRT

<213> Ovis aries

<400> 17

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
 1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu
 20 25 30

Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe
 35 40 45

Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
 50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
 65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr
 100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
 115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
 130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr
 145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
 165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
 195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
 210 215 220

Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
 260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
 290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
 305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg
 325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
 340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg
 370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn
 385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
 420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp
 435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp
 450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn
 465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu
 485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly
 500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr
 515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln
 530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
 660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val
 705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
 725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
 755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
 785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
 805 810 815

Phe Gly Phe Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met
 820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys
 835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu
 850 855 860

Leu Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val Ala
 865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly
 885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly
 900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys
 915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg

930 935 940
 Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp
 945 950 955 960
 Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr
 965 970 975
 Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro
 980 985 990
 His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Met Ala
 995 1000 1005
 Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg
 1010 1015 1020
 Gly Pro Thr Thr Ala Glu
 1025
 <210> 18
 <211> 818
 <212> PRT
 <213> Ovis aries
 <400> 18
 Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
 1 5 10 15
 Ala Ala Leu Ala Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu
 20 25 30
 Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe
 35 40 45
 Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
 50 55 60
 Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
 65 70 75 80
 Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
 85 90 95
 Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr

100	105	110
Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn		
115	120	125
Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu		
130	135	140
Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr		
145	150	155
His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn		
165	170	175
Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly		
180	185	190
Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn		
195	200	205
Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu		
210	215	220
Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala		
225	230	235
Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg		
245	250	255
Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro		
260	265	270
Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu		
275	280	285
Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg		
290	295	300
Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr		
305	310	315
Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg		
325	330	335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
 340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg
 370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn
 385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
 420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp
 435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp
 450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn
 465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu
 485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly
 500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr
 515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln
 530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
 660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val
 705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
 725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
 755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
 785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
 805 810 815

Phe Gly

<210> 19

<211> 3199

<212> DNA

<213> *Ovis aries*

<400> 19

```

gtcggcacgg gaagtgagcg ccaagcatcc ttccctgcag ctgccgcca acttgcccgc      60
cagaccctct ggagaagcgg cattccctgc catggggccc tactgtgccc cgcaccccct      120
ttctctcctg gtgcaggcgg cggcgctggc agcagccctg gcccagggca ccctgcctgc      180
cttcctgccc tgtgagctcc agccccgggg taagggtgaac tgcaactggc tgttcctgaa      240
gtctgtgccc cgcttttcgg cgggagcccc cggggccaat gtcaccagcc tctccttaat      300
ctccaaccgc atccaccact tgcacgactc tgacttcgtc cacctgtcca acctgcggggt      360
cctcaacctc aagtggaaact gcccgccggc cggcctcagc cccatgcact tcccctgccc      420
catgaccatc gagcccaaca ccttcctggc tgtgccacc ctggaggagc tgaacctgag      480
ctacaatggc atcacgaccg tgcttgcct gccagttct ctcttatccc tgtcgtgag      540
ccgcaccagc atcctggtgc taggccccac ccacttcacc ggcttgcacg ccctgcgctt      600
tctgtacatg gagcgcaact gctactataa gaacccctgc cagcaggccg tggagggtggc      660
cccaggcgcc ctcttgggc tgggcaacct cagcacctg tcgctcaagt acaacaacct      720
cacggagggtg ccccgccgcc tgccccccag cctggacacc ctgctgctgt cctacaacca      780
catcatcacc ctggcaccgg aggacctggc caatctgact gccctgcgtg tgcttgatgt      840
ggggcggaac tgccgcgct gcgaccacgc ccgcaacccc tgcagggagt gcccagaaga      900
cttccccaag ctgcacctg acaccttcag ccacctgagc cgcctcgaag gcctggtgtt      960
gaaggacagt tctctctaca aactagagaa agactggttc cgcggcctgg gcaggctcca     1020
agtgtctgac ctgagtgaga acttcctcta tgactacatc accaagacca ccatcttcag     1080
gaacctgacc cagctgcgca gactcaacct gtccctcaat taccacaaga aggtgtcctt     1140
cgcccacctg caactggcac cctcctttgg gggcctgggtg tccttgaga agctggacat     1200
gcacggcatc ttcttcgct cctcaccaa caccacgctc cggccgctga ccagctgcc     1260
caagctccag agtctgagtc tgcagctgaa cttcatcaac caggccgagc tcagcatctt     1320
tggggccttc ccgagcctgc tcttcgtgga cctgtcggac aaccgcatca gcggagctgc     1380
gaggccggtg gccgccctcg gggagggtgga cagcggggtg gaagtctggc ggtggcccag     1440

```

gggcctcgct ccaggccgc tggccgccgt cagcgcaaag gacttcacgc caagctgcaa 1500
 cctcaacttc accttgacc tgtcacggaa caacctggtg acgatccagc aggagatgtt 1560
 taccgcctc tccgcctcc agtgccctgc cctgagccac aacagcatct cgcaggcgggt 1620
 taatggctcg cagttcgtgc cgctgaccgc cctgagctg ctgcacctgt cctacaaca 1680
 gctggacctg taccatgggc gctcgttcac ggagctgccg cagctggagg cactggacct 1740
 cagctacaac agccagccct tcagcatgca gggcgtaggc cacaacctca gtttcgtggc 1800
 ccagctgccg tccctgcgt acctcagcct tgcgcacaac ggcatccaca gccgcgtgtc 1860
 acagaagctc agcagcgccct cgctgcgcgc cctggacttc agcggcaact ccctgagcca 1920
 gatgtgggcc gagggagacc tctatctctg cttcttcaaa ggcttgagga acctgggtcca 1980
 gctggacctg tccaagaacc acctgcacac cctcctgcct cgtcacctgg ataacctgcc 2040
 caagagcctg cggcagctgc gtctccggga caataacctg gccttcttca actggagcag 2100
 cctgactgtt ctgccccagc tggagccct ggatctggcg ggaaaccagc tgaaggccct 2160
 gagcaacggc agcctgccac ctggcaccgc gctccagaag ctggacgtga gcagcaacag 2220
 catcggttt gtgaccctg gcttcttctg ccttgccaac cggctgaaag agcttaacct 2280
 cagcgccaac gccctgaaga cagtggatcc cttctggttc ggtcgcttaa cagagacct 2340
 gaataccta gacgtgagcg ccaaccgcct ccactgtgcc tgcggggcgg cctttgtgga 2400
 cttcctgctg gagatgcagg cggccgtgcc tgggctgtcc aggcgcgtca cgtgtggcag 2460
 tccgggccag ctccagggcc gcagcatctt cgcacaggac ctgcgcctct gcctggatga 2520
 gacctctctc ttggactgct ttggcttctc gctgctaata gtggcgctgg gcctggcgggt 2580
 gccatgctg caccacctct gtggctggga cctgtggtac tgcttccacc tgtgtctggc 2640
 ccatttgccc cgacggcggc ggcagcgggg cgaggacacc ctgctctacg atgccttctg 2700
 ggtcttcgac aaggcgcaga gtgcagtggc cgactgggtg tacaacgagc tccgcgtgca 2760
 gctggaggag cgccgcgggc gccgggcgct ccgcctctgc ctggaggagc gagactggct 2820
 ccctggcaag acgctcttcg agaacctgtg ggcctcggtc tacagcagcc gtaagaccat 2880
 gttcgtgctg gaccacacgg accgggtcag tggcctcctg cgcgccagct tctgctggc 2940
 ccagcagcgc ctgttgagg accgcaagga tgcgtggtg ctggtgatcc tgcgccccgc 3000
 cgcctaccgg tcccgctacg tgcggctgcg ccagcgcctc tgccgccaga gcgtcctcct 3060
 ctggccccac cagcccagtg gccagggtag cttctggggc aacctgggca tggccctgac 3120
 cagggacaac cgccacttct ataaccggaa cttctgccgg ggccccacga cagccgaata 3180

gcacagagtg actgcccag

3199

<210> 20

<211> 2454

<212> DNA

<213> Ovis aries

<400> 20

atgggcccct actgtgcccc gcacccccctt tctctcctgg tgcaggcggc ggcgctggca 60

gcagccctgg ccagggcac cctgcctgcc ttctgccct gtgagctcca gcccgggggt 120

aaggatgaact gcaactggct gttcctgaag tctgtgccgc gcttttcggc cggagccccc 180

cgggccaatg tcaccagcct ctcccttaate tccaaccgca tccaccactt gcacgactct 240

gacttcgtcc acctgtccaa cctgcgggtc ctcaacctca agtggaaactg cccgcccggc 300

ggcctcagcc ccatgcactt cccctgccgc atgaccatcg agcccaacac ctctctggct 360

gtgcccaccc tggaggagct gaacctgagc tacaatggca tcacgaccgt gcctgccctg 420

cccagttctc tcgtatccct gtcgctgagc cgcaccagca tcttggtgct agggcccacc 480

cacttcaccg gcctgcacgc cctgcgcttt ctgtacatgg acggcaactg ctactataag 540

aaccctgcc agcaggccgt ggaggtggcc ccaggcgccc tccttggcct gggcaacctc 600

acgcacctgt cgctcaagta caacaacctc acggaggtgc cccgcccgcct gccccccagc 660

ctggacaccc tgctgctgtc ctacaaccac atcatcacc tggcaccoga ggacctggcc 720

aatctgactg ccctgcgtgt gcttgatgtg ggcggaact gccgcccgtg cgaccacgcc 780

cgcaaccctt gcagggagtg cccaaagaac ttccccaagc tgcaccctga caccttcagc 840

cacctgagcc gcctcgaagg cctggtgttg aaggacagtt ctctctacaa actagagaaa 900

gactggttcc ggggcctggg caggtccaa gtgctcgacc tgagtgagaa ctctctctat 960

gactacatca ccaagaccac catcttcagg aacctgacct agctgcgcag actcaacctg 1020

tccttcaatt accacaagaa ggtgtccttc gccacctgc aactggcacc ctcttttggg 1080

ggcctggtgt ccctggagaa gctggacatg cacggcatct tcttccgctc cctcaccaac 1140

accacgctcc ggccgctgac ccagctgccc aagctccaga gtctgagtct gcagctgaac 1200

ttcatcaacc aggcgagct cagcatcttt ggggccttcc cgagcctgct ctctgtggac 1260

ctgtcggaca accgcatcag cggagctgcg aggcgggtgg ccgcccctgg ggaggtggac 1320

agcgggggtg aagtctggcg gtggcccagg ggcctcgctc caggcccgct ggccgcccgc 1380

agcgcgaaagg acttcatgcc aagctgcaac ctcaacttca ccttggacct gtcacggaac 1440

aacctggtga cgatccagca ggagatgttt acccgccctc cccgcctcca gtgcctgcgc 1500

ctgagccaca acagcatctc gcaggcgggtt aatggctcgc agttcgtgcc gctgacccgc 1560
 ctgcgagtgc tcgacctgtc ctacaacaag ctggacctgt accatgggcg ctcgttcacg 1620
 gagctgccgc agctggaggc actggacctc agctacaaca gccagccctt cagcatgcag 1680
 ggcgtgggcc acaacctcag ctctgtggcc cagctgccgt ccctgcgcta cctcagcctt 1740
 gcgcacaacg gcatccacag ccgcgtgtca cagaagctca gcagcgcctc gctgcgcgcc 1800
 ctggacttca ggggcaactc cctgagccag atgtggggcg agggagacct ctatctctgc 1860
 ttcttcaaag gcttgaggaa cctgggtccag ctggacctgt ccaagaacca cctgcacacc 1920
 ctctgcctc gtcacctgga taacctgccc aagagcctgc ggcagctgcg tctccgggac 1980
 aataacctgg ctttcttcaa ctggagcagc ctgactgttc tgccccagct ggaagccctg 2040
 gatctggcgg gaaaccagct gaaggccctg agcaacggca gcctgccacc tggcaccg 2100
 ctccagaagc tggacgtgag cagcaacagc atcggtttt tgacccttg cttctttgtc 2160
 cttgccaacc ggctgaaaga gcttaacctc agcgccaacg ccctgaagac agtggatccc 2220
 ttctggttcg gtcgcttaac agagaccctg aatatcctag acgtgagcgc caaccgctc 2280
 cactgtgcct gcggggcgcc ctttgtggac ttcctgctgg agatgcaggc ggccgtgcct 2340
 gggctgtcca ggcgcgtcac gtgtggcagt ccgggccagc tccagggccg cagcatcttc 2400
 gcacaggacc tgcgcctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 21
 <211> 1032
 <212> PRT
 <213> Canis familiaris

<400> 21

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
 65 70 75 80

Tyr	Asp	Phe	Val	His	Phe	Val	His	Leu	Arg	Arg	Leu	Asn	Leu	Lys	Trp
				85					90					95	
Asn	Cys	Pro	Pro	Ala	Ser	Leu	Ser	Pro	Met	His	Phe	Pro	Cys	His	Met
			100					105					110		
Thr	Ile	Glu	Pro	Asn	Thr	Phe	Leu	Ala	Val	Pro	Thr	Leu	Glu	Asp	Leu
		115					120					125			
Asn	Leu	Ser	Tyr	Asn	Ser	Ile	Thr	Thr	Val	Pro	Ala	Leu	Pro	Ser	Ser
	130					135					140				
Leu	Val	Ser	Leu	Ser	Leu	Ser	Arg	Thr	Asn	Ile	Leu	Val	Leu	Asp	Pro
145					150					155					160
Ala	Thr	Leu	Ala	Gly	Leu	Tyr	Ala	Leu	Arg	Phe	Leu	Phe	Leu	Asp	Gly
				165					170					175	
Asn	Cys	Tyr	Tyr	Lys	Asn	Pro	Cys	Gln	Gln	Ala	Leu	Gln	Val	Ala	Pro
			180					185					190		
Gly	Ala	Leu	Leu	Gly	Leu	Gly	Asn	Leu	Thr	His	Leu	Ser	Leu	Lys	Tyr
		195					200					205			
Asn	Asn	Leu	Thr	Val	Val	Pro	Arg	Gly	Leu	Pro	Pro	Ser	Leu	Glu	Tyr
	210					215					220				
Leu	Leu	Leu	Ser	Tyr	Asn	His	Ile	Ile	Thr	Leu	Ala	Pro	Glu	Asp	Leu
225					230					235					240
Ala	Asn	Leu	Thr	Ala	Leu	Arg	Val	Leu	Asp	Val	Gly	Gly	Asn	Cys	Arg
				245					250					255	
Arg	Cys	Asp	His	Ala	Arg	Asn	Pro	Cys	Arg	Glu	Cys	Pro	Lys	Gly	Phe
			260					265					270		
Pro	Gln	Leu	His	Pro	Asn	Thr	Phe	Gly	His	Leu	Ser	His	Leu	Glu	Gly
		275					280					285			
Leu	Val	Leu	Arg	Asp	Ser	Ser	Leu	Tyr	Ser	Leu	Asp	Pro	Arg	Trp	Phe
	290					295					300				
His	Gly	Leu	Gly	Asn	Leu	Met	Val	Leu	Asp	Leu	Ser	Glu	Asn	Phe	Leu
305					310					315					320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
 340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
 355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu
 370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu
 385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu
 420 425 430

Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val
 435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly
 450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp
 465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg
 485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln
 500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu
 515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr
 530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro

545	550	555	560
Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu	565	570	575
Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg	580	585	590
Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser	595	600	605
Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg	610	615	620
Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn	625	630	635
Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser	645	650	655
Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp	660	665	670
Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly	675	680	685
Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln	690	695	700
Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro	705	710	715
Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala	725	730	735
Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly	740	745	750
Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys	755	760	765
Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro	770	775	780

Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly
785 790 795 800

Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu
805 810 815

Ser Trp Val Cys Phe Ser Leu Ser Leu Leu Ala Val Ala Leu Ser Leu
820 825 830

Ala Val Pro Met Leu His Gln Leu Cys Gly Trp Asp Leu Trp Tyr Cys
835 840 845

Phe His Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Arg Gly
850 855 860

Val Asp Ala Leu Ala Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln
865 870 875 880

Ser Ser Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu
885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp
900 905 910

Trp Val Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr
915 920 925

Ser Ser Arg Lys Thr Leu Phe Val Leu Ala Arg Thr Asp Arg Val Ser
930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Cys Pro Asp Ala His
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln
995 1000 1005

Leu Gly Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln
1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Thr Ala
1025 1030

<210> 22
<211> 822
<212> PRT
<213> Canis familiaris

<400> 22

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn
50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
65 70 75 80

Tyr Asp Phe Val His Phe Val His Leu Arg Arg Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Asp Leu
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
145 150 155 160

Ala Thr Leu Ala Gly Leu Tyr Ala Leu Arg Phe Leu Phe Leu Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Leu Gln Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Val Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Gly Phe
 260 265 270

Pro Gln Leu His Pro Asn Thr Phe Gly His Leu Ser His Leu Glu Gly
 275 280 285

Leu Val Leu Arg Asp Ser Ser Leu Tyr Ser Leu Asp Pro Arg Trp Phe
 290 295 300

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
 340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
 355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu
 370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu
 385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu
 420 425 430

Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val
 435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly
 450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp
 465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg
 485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln
 500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu
 515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr
 530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro
 545 550 555 560

Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu
 565 570 575

Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg
 580 585 590

Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser
 595 600 605

Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg
 610 615 620

Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn
 625 630 635 640

Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser
 645 650 655

Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp

660 665 670
 Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly
 675 680 685
 Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln
 690 695 700
 Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro
 705 710 715 720
 Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala
 725 730 735
 Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly
 740 745 750
 Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys
 755 760 765
 Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro
 770 775 780
 Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly
 785 790 795 800
 Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu
 805 810 815
 Ser Trp Val Cys Phe Ser
 820

<210> 23
 <211> 3334
 <212> DNA
 <213> Canis familiaris

<400> 23
 aggaaggggc tgtgagctcc aagcatcctt tcctgcagct gctgcccagc ctgccagcca 60
 gaccctctgg agaagcccc gctccctgtc atgggcccct gccgtggcgc cctgcacccc 120
 ctgtctctcc tgggtgcaggc tgccgcgcta gccctggccc tggcccaggg caccctgcct 180
 gccttcctgc cctgtgagct ccagcccat ggctgtgga actgcaactg gctgttcctc 240
 aagtccgtgc cccgcttctc ggcagctgca cccgcggta acgtcaccag cctttccttg 300

tactccaacc gcatccacca cctccatgac tatgactttg tccacttcgt ccacctgcgg	360
cgtctcaatc tcaagtggaa ctgcccgcgc gccagcctca gcccacatgca ctttccctgt	420
cacatgacca ttgagcccaa caccttcctg gctgtgcca ccctagagga cctgaatctg	480
agctataaca gcatcacgac tgtgcccgc ctgcccagtt cgcttggtgc cctgtccctg	540
agccgcacca acatcctggt gctggaccct gccaccctgg caggccttta tgccctgcgc	600
ttcctgttcc tggatggcaa ctgctactac aagaaccctt gccagcaggc cctgcagggtg	660
gcccaggtg ccctcctggg cctgggcaac ctcacacacc tgctactcaa gtacaacaac	720
ctcaccgtgg tgccgcgggg cctgcccccc agcctggagt acctgctctt gtccctacaac	780
cacatcatca ccctggcacc tgaggacctg gccaatctga ctgccctgcg tgtccctgat	840
gtgggtggga actgtcgccg ctgtgacct gcccgtaacc cctgcaggga gtgccccaa	900
ggcttcccc agctgcacc caacaccttc ggccacctga gccacctga aggcctggtg	960
ttgagggaca gctctctcta cagcctggac ccaggtggt tccatggcct gggcaacctc	1020
atggtgctgg acctgagtga gaacttcctg tatgactgca tcacaaaaac caaagccttc	1080
tacggcctgg ccgggtgcg cagactcaac ctgtccttca attatcataa gaagggtgtc	1140
tttgcccacc tgcatctggc atcctccttc gggagcctac tgtccctgca ggagctggac	1200
atacatggca tcttcttccg ctgctcagc aagaccacgc tccagtcgtt gggccacctg	1260
cccatgctcc agcgtctgca tctgcagttg aactttatca gccaggccca gctcagcatc	1320
ttcggcgcct tccctggact gcggtacgtg gacttgtcag acaaccgcat cagtggagct	1380
gcagagcccg cggctgccac aggggaggta gaggcagact gtggggagag agtctggcca	1440
cagtcceggg accttgctct gggcccactg ggcaccccg gctcagaggc ctccatgccg	1500
agctgcagga ccctcaactt caccttgga ctgtctcgga acaacctagt gactgttcag	1560
ccggagatgt ttgtccggct ggcgcgcctc cagtgcctgg gcctgagcca caacagcatc	1620
tcgcaggcgg tcaatggctc gcagttcgtg cctctgagca acctgcgggt gctggacctg	1680
tcccataaca agctggacct gtaccacggg cgctcgttca cggagctgcc gcggtggag	1740
gccttggaac tcagctacaa cagccagccc ttcagcatgc ggggcgtggg ccacaatctc	1800
agctttgtgg cacagctgcc agccctgcgc tacctcagcc tggcgcaaa tggcatccac	1860
agccgcgtgt cccagcagct ccgcagcgcc tcgctccggg ccctggactt cagtggcaat	1920
accctgagcc agatgtgggc cgaggagac ctctatctcc gcttcttcca aggctgaga	1980
agcctgggtc agctggacct gtcccagaat cgctgcata ccctcctgcc acgcaacctg	2040
gacaacctcc ccaagagcct gcggctcctg cggctccgtg acaattacct ggctttcttc	2100

aactggagca gcctggccct cctaccaag ctggaagccc tggacctggc gggaaaccag 2160
ctgaaggccc tgagcaatgg cagcttgccc aacggcacc agctccagag gctggacctc 2220
agcggcaaca gcatcggtt cgtggtcccc agcttttttg ccctggcgt gaggttcga 2280
gagctcaacc tcagcgcaa cgccctcaag acggtggagc cctcctggtt tggttccctg 2340
gcgggtgccc tgaaagtcct agacgtgacc gccaacccct tgcattgcgc ttgcggcgca 2400
accttcgtgg acttcttgct ggaggtgcag gctgcggtgc ccggcctgcc tagccgtgtc 2460
aagtgcggca gcccgggcca gctccaggc cgcagcatct tcgcacagga cctgcgcctc 2520
tgcttgagc aagcgtctc ctgggtctgt ttcagcctct cgctgctggc tgtggccctg 2580
agcctggctg tgcccatgct gcaccagctc tgtggctggg acctctggta ctgcttcac 2640
ctgtgcctgg cctggctgcc ccggcggggg cggcggggg gtgtggatgc cctggcctat 2700
gacgccttcg tggcttcga caaggcgcag agctcgggtg cggactgggt gtacaatgag 2760
ctgcgggtac agctagagga gcgcgtggg cgcgggggc tacgcctgtg tctggaggaa 2820
cgtgactggg taccggcaa aacctcttc gagaacctct gggcctcagt ttacagcagc 2880
cgcaagacgc tgtttgtgct ggcccgacg gacagagtca gcggcctcct gcgtgccagc 2940
ttcctgctgg cccaacagcg cctgctggag gaccgcaagg acgtcgtggg gctggtgatc 3000
ctgtgccccg acgcccaccg ctcccgtat gtgcggctgc gccagcgct ctgccgccag 3060
agtgtcctcc tctggcccca ccagccaggt ggccagcgca gcttctgggc ccagctgggc 3120
acggccctga ccagggacaa ccgccacttc tacaaccaga acttctgccg gggccccacg 3180
acagcctgat aggcagacag ccagcacct tcgcgcccct acaccctgcc tgtctgtctg 3240
ggatgcccga cctgctggct ctacaccgcc gctctgtctc ccctacacc agccctggca 3300
taaagcgacc gctcaataaa tgctgctggg agac 3334

<210> 24

<211> 2466

<212> DNA

<213> Canis familiaris

<400> 24

atgggcccct gccgtggcg cctgcacccc ctgtctctcc tggcagggc tgccgcgcta 60
gccctggccc tggcccaggg caccctgcct gccttcctgc cctgtgagct ccagcccat 120
ggcctgggtga actgcaactg gctgttcctc aagtcctgct cccgcttctc ggcagctgca 180
ccccgggta acgtcaccag cctttccttg tactccaacc gcatccacca cctccatgac 240
tatgactttg tccacttcgt ccacctggg cgtctcaatc tcaagtggaa ctgcccggcc 300

gccagcctca gcccacatgca ctttccctgt cacatgacca ttgagcccaa caccttcctg 360
 gctgtgcccc ccctagagga cctgaatctg agctataaca gcatcacgac tgtgccccgcc 420
 ctgcccagtt cgcttgtgtc cctgtccctg agccgcacca acatcctggg gctggaccct 480
 gccaccctgg caggccttta tgccctgcgc ttctgttcc tggatggcaa ctgctactac 540
 aagaaccctt gccagcagga cctgcaggtg gcccaggtg ccctcctggg cctgggcaac 600
 ctcacacacc tgtcactcaa gtacaacaac ctaccctggg tgccgcgggg cctgcccccc 660
 agcctggagt acctgtctt gtctacaac cacatcatca ccctggcacc tgaggacctg 720
 gccaatctga ctgcccctgcg tgcctcgat gtgggtggga actgtcgccg ctgtgacct 780
 gcccgtaac cctgcagga gtgcccacag ggcttcccc agctgcacc caacaccttc 840
 ggccacctga gccacctga aggcctgggt ttgaggga gctctctcta cagcctggac 900
 cccaggtggg tccatggcct gggcaacctc atgggtgctg acctgagtga gaacttcctg 960
 tatgactgca tcacaaaac caaagccttc tacggcctgg ccggctgcg cagactcaac 1020
 ctgtccttca attatcataa gaaggtgtcc tttgccacc tgcatctggc atcctccttc 1080
 gggagcctac tgtccctgca ggagctggac atacatggca tcttcttccg ctgctcagc 1140
 aagaccagc tccagtcgct ggccacctg cccatgctcc agcgtctgca tctgcagttg 1200
 aactttatca gccaggccca gctcagcatc ttggcgccct tccctggact gcggtacgtg 1260
 gacttgtcag acaaccgcat cagtggagct gcagagccc cggtgccac aggggaggt 1320
 gaggcagact gtggggagag agtctggcca cagtcccggg acctgtctt gggccactg 1380
 ggcacccccg gctcagaggc cttcatgcc agctgcagga ccctcaactt caccttggac 1440
 ctgtctcgga acaacctagt gactgttcag ccggagatgt ttgtccggct ggcggcctc 1500
 cagtgcctgg gcctgagcca caacagcatc tcgcaggcgg tcaatggctc gcagttcgtg 1560
 cctctgagca acctgcgggt gctggacctg tcccataaca agctggacct gtaccaggg 1620
 cgctcgttca cggagctgcc gcggctggag gccttgacc tcagctaaa cagccagccc 1680
 ttcagcatgc ggggcgtggg ccacaatctc agctttgtgg cacagctgcc agccctgcgc 1740
 tacctcagcc tggcgacaaa tggcatccac agccgcgtgt cccagcagct ccgcagcgcc 1800
 tcgctccggg ccctggactt cagtggcaat accctgagcc agatgtgggc cgaggagac 1860
 ctctatctcc gcttcttcca aggcctgaga agcctggttc agctggacct gtoccagaat 1920
 cgctgcata ccctcctgcc acgcaacctg gacaacctcc ccaagagcct gcggctcctg 1980
 cggtccgtg acaattacct ggctttcttc aactggagca gcctggccct cctaccaag 2040

ctggaagccc tggacctggc gggaaaccag ctgaaggccc tgagcaatgg cagcttgccc 2100
 aacggcaccc agctccagag gctggacctc agcggcaaca gcatcggett cgtggtcccc 2160
 agcttttttg ccctggccgt gaggttcga gagctcaacc tcagcgccaa cgccctcaag 2220
 acggtggagc cctcctgggt tggttccctg gcgggtgccc tgaaagtctt agacgtgacc 2280
 gccaacccct tgcattgcgc ttgcggcgca accttcgtgg acttcttgct ggaggtgcag 2340
 gctgcggtgc ccggcctgcc tagccgtgtc aagtgcggca gcccgggcca gctccagggc 2400
 cgcagcatct tcgcacagga cctgcgcctc tgcttgagc aagcgtctc ctgggtctgt 2460
 ttcagc 2466

<210> 25
 <211> 1031
 <212> PRT
 <213> Felis catus

<400> 25

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
 20 25 30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Pro Arg Gly Asn
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
 65 70 75 80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
 100 105 110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
 115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
 130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
 145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe
 260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe
 290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
 340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu
 370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu
 420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu
 435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu
 450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser
 465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser
 485 490 495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val
 500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
 515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
 530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
 545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala
 565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser
 580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
 595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe

610				615				620							
Arg 625	Gly	Leu	Arg	Ser	Leu 630	Val	Arg	Leu	Asp	Leu 635	Ser	Gln	Asn	Arg	Leu 640
His	Thr	Leu	Leu	Pro 645	Arg	Thr	Leu	Asp	Asn 650	Leu	Pro	Lys	Ser	Leu 655	Arg
Leu	Leu	Arg	Leu 660	Arg	Asp	Asn	Tyr	Leu 665	Ala	Phe	Phe	Asn	Trp 670	Ser	Ser
Leu	Val	Leu 675	Leu	Pro	Arg	Leu	Glu 680	Ala	Leu	Asp	Leu	Ala 685	Gly	Asn	Gln
Leu	Lys 690	Ala	Leu	Ser	Asn 695	Gly	Ser	Leu	Pro	Asn 700	Gly	Thr	Gln	Leu	Gln
Arg 705	Leu	Asp	Leu	Ser	Ser 710	Asn	Ser	Ile	Ser	Phe 715	Val	Ala	Ser	Ser	Phe 720
Phe	Ala	Leu	Ala	Thr 725	Arg	Leu	Arg	Glu 730	Leu	Asn	Leu	Ser	Ala 735	Asn	Ala
Leu	Lys	Thr	Val 740	Glu	Pro	Ser	Trp	Phe 745	Gly	Ser	Leu	Ala	Gly 750	Thr	Leu
Lys	Val 755	Leu	Asp	Val	Thr	Gly	Asn 760	Pro	Leu	His	Cys	Ala 765	Cys	Gly	Ala
Ala 770	Phe	Val	Asp	Phe	Leu	Leu 775	Glu	Val	Gln	Ala	Ala 780	Val	Pro	Gly	Leu
Pro 785	Gly	His	Val	Lys	Cys 790	Gly	Ser	Pro	Gly	Gln 795	Leu	Gln	Gly	Arg	Ser 800
Ile	Phe	Ala	Gln	Asp 805	Leu	Arg	Leu	Cys	Leu 810	Asp	Glu	Ala	Leu 815	Ser	Trp
Asp	Cys	Phe	Gly 820	Leu	Ser	Leu	Leu	Thr 825	Val	Ala	Leu	Gly	Leu 830	Ala	Val
Pro	Met	Leu 835	His	His	Leu	Cys	Gly 840	Trp	Asp	Leu	Trp	Tyr 845	Cys	Phe	His

Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Arg Gly Ala Asp
 850 855 860

Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala
 865 870 875 880

Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg
 885 890 895

Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu
 900 905 910

Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser
 915 920 925

Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu
 930 935 940

Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg
 945 950 955 960

Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His Arg Ser
 965 970 975

Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu
 980 985 990

Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly
 995 1000 1005

Thr Ala Leu Thr Arg Asp Asn Gln His Phe Tyr Asn Gln Asn Phe
 1010 1015 1020

Cys Arg Gly Pro Thr Thr Ala Glu
 1025 1030

<210> 26

<211> 820

<212> PRT

<213> Felis catus

<400> 26

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
 20 25 30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
 65 70 75 80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
 100 105 110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
 115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
 130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
 145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe
 260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe
 290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
 340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu
 370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu
 420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu
 435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu
 450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser
 465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser
 485 490 495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala
565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser
580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe
610 615 620

Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg
645 650 655

Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
660 665 670

Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln
675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln
690 695 700

Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe
705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala

725 730 735
 Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu
 740 745 750
 Lys Val Leu Asp Val Thr Gly Asn Pro Leu His Cys Ala Cys Gly Ala
 755 760 765
 Ala Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
 770 775 780
 Pro Gly His Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
 785 790 795 800
 Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
 805 810 815
 Asp Cys Phe Gly
 820

<210> 27
 <211> 3235
 <212> DNA
 <213> Felis catus

<400> 27
 aggggtctgcg agctccaggc attcttctct gccatcgctg cccagtctgc catccagacc 60
 ctctggagaa gccccactc cctgtcatgg gcccctgcca tggcgccctg caccctctgt 120
 ctctcctggt gcaggctgcc gcgctggccg tggccctggc ccagggcacc ctgcctgcct 180
 ttctgccttg tgagctccag cgccacggcc tgggtgaattg cgactggctg ttcctcaagt 240
 ccgtgccccca cttctcggcg gcagcgcccc gtggtaacgt caccagcctt tccctgtact 300
 ccaaccgcat ccaccacctc cactgactccg actttgtcca cctgtccagc ctgcggcgctc 360
 tcaacctcaa atggaactgc ccaccgcca gcctcagccc catgcacttc ccctgtcaca 420
 tgaccattga gccccacacc ttcttgccg tgcccaccct ggaggagctg aacctgagct 480
 acaacagcat cactgacagta ccgcccctgc ccagttccct cgtgtccctg tccttgagcc 540
 gtaccaacat cctggtgctg gaccctgcca acctcgagg gctgcactcc ctgcgctttc 600
 tgttcttgga tggcaactgc tactacaaga acccctgccc gcaggccctg cagggtggccc 660
 cgggcgccct ccttggcctg ggcaacctta cgcacctgtc actcaagtac aacaacctca 720
 ctgcggtgcc ccgcgccctg cccccagcc tggagtacct gctattgtcc tacaaccaca 780

tcataccacct	ggcacctgag	gacctggcca	acctgaccgc	cctgcgtgtg	ctcgatgtgg	840
gtgggaactg	ccgtcgctgt	gaccacgccc	gcaaccctg	tatggagtgc	cccaagggct	900
ttccgcacct	gcaccctgac	accttcagcc	acctgaacca	cctcgaaggc	ctgggtgtga	960
aggacagctc	tctctacaac	ctgaacccca	gatggttcca	tgccctgggc	aacctcatgg	1020
tgctggacct	gagtgagaac	ttcctatatg	actgcatcac	caaaaccaca	gccttccagg	1080
gcctggccca	gctgcgcaga	ctcaacttgt	ctttcaatta	ccacaagaag	gtgtcctttg	1140
cccacctgca	tctggcgccc	tccttcggga	gcctgctctc	cctgcagcag	ctggacatgc	1200
atggcatctt	cttcgcgtcg	ctcagcgaga	ccacgctccg	gtcgctggtc	cacctgcccc	1260
tgctccagag	tctgcacctg	cagatgaact	tcataaatca	ggcccagctc	agcatcttcg	1320
gggccttccc	tggcctgcga	tacgtggacc	tgtcagacaa	ccgcataagt	ggagccatgg	1380
agctggcggc	tgccacgggg	gaggtggatg	gtggggagag	agtccggctg	ccatctgggg	1440
acctagctct	gggcccaccg	ggcacccta	gctccgaggg	cttcatgcca	ggctgcaaga	1500
ccctcaactt	caccttggac	ctgtcacgga	acaacctagt	gacaatccag	ccagagatgt	1560
ttgcccggct	ctcgcgctc	cagtgcctgc	tcctgagccg	caacagcatc	tcgcaggcag	1620
tcaacggctc	acaatttatg	ccgctgacca	gcctgcaggt	gctggacctg	tcccataaca	1680
agctggacct	gtaccatggg	cgctctttca	cggagctgcc	gcggctggag	gccctggacc	1740
tcagctacaa	cagccagccc	ttcagcatgc	agggcgctgg	tcacaacctc	agctttgtgg	1800
cacagctgcc	ggccctgcgc	tatctcagcc	tggcgcacaa	cgacatccac	agccgtgtgt	1860
cccagcagct	ctgcagcgcc	tcgctgcggg	ccttggactt	cagcggcaat	gccttgagcc	1920
ggatgtgggc	cgaggggagac	ctgtatctcc	acttcttccg	aggcctgagg	agcctggtcc	1980
ggttggatct	gtcccagaat	cgctgcata	ccctcttgcc	acgcaccctg	gacaacctcc	2040
ccaagagcct	gcggctgctg	cgtctccgtg	acaattatct	ggctttcttc	aactggagca	2100
gcctggtcct	cctccccagg	ctggaagccc	tggacctggc	gggaaaccag	ctgaaggccc	2160
tgagcaacgg	cagcttgcc	aatggaaccc	agctccagag	gctggacctc	agcagcaaca	2220
gtatcagctt	cgtggcctcc	agcttttttg	ctctggccac	caggctgcga	gagctcaacc	2280
tcagtgccaa	cgccctcaag	acggtggagc	cctcctgggt	cggttctcta	gcgggcaccc	2340
tgaaagtcc	agatgtgact	ggcaaccccc	tgcactgcgc	ctgtggggcg	gccttcgtgg	2400
acttcttgct	ggaggtgcag	gctgcagtgc	ccggcctgcc	aggccacgct	aagtgtggca	2460
gtccaggtca	gtccagggc	cgcagcatct	ttgcgcagga	tctgcgctc	tgcttgatg	2520
aggccctctc	ctgggactgt	tttggcctct	cgctgctgac	cgtggccctg	ggcctggccg	2580

tgcccatgct gcaccacctc tgtggctggg acctctggta ctgcttcac ctgtgcctgg 2640
 cctggctgcc cggcgggggg cggcgggggg gcgcggatgc cctgccctac gatgcctttg 2700
 tggctcttcga caaggcacag agcgcgggtg cgcactgggt gtacaacgag ctgcgggtac 2760
 ggctagagga gcgcctgga cgcgagcgc tccgcctgtg cctggaggaa cgtgactggc 2820
 taccggtaa aacgctcttt gagaacctgt gggcctcagt ttacagcagc cgcaagatgc 2880
 tgtttgtgct ggccacaca gacaggggtca gcggcctctt gcgcgccagc tttctgctgg 2940
 cccagcagcg cctgctggag gaccgcaagg acgttgtggg gctgggtgatc ctgcgccccg 3000
 acgcccaccg ctcccgctat gtgcggctgc gccagcgcct ctgccgccag agcgtcctcc 3060
 tctggccccca ccagcccagt ggcagcgcga gcttctgggc ccagctgggc acggccctga 3120
 ccagggacaa ccagcacttc tataaccaga acttctgccg gggccccacg acggcagagt 3180
 gaccgccag caccccaagc ctctacacc ttgcctgtct gcctgggatg ccggg 3235

<210> 28

<211> 2460

<212> DNA

<213> *Felis catus*

<400> 28

atgggcccct gccatggcgc cctgcacccc ctgtctctcc tggcgcaggc tgccgcgctg 60
 gccgtggccc tggcccaggg caccctgcct gcctttctgc cctgtgagct ccagcgccac 120
 ggcctgggtga attgcgactg gctgttcctc aagtcctgac cccacttctc ggcggcagcg 180
 ccccgctggta acgtcaccag cctttccctg tactccaacc gcattcacca cctccacgac 240
 tccgactttg tccacctgtc cagcctgcgg cgtctcaacc tcaaattgaa ctgcccaccc 300
 gccagcctca gcccctatgca cttcccctgt cacatgacca ttgagcccca caccttctg 360
 gccgtgcccc ccctggagga gctgaacctg agctacaaca gcattcacgac agtaccgcgc 420
 ctgcccagtt ccctcgtgtc cctgtccttg agccgtacca acatcctggg gctggaccct 480
 gccaacctcg cagggtgca ctccctgcgc tttctgttcc tggatggcaa ctgctactac 540
 aagaaccctt gccgcaggc cctgcagggt gcccggggcg ccctccttgg cctgggcaac 600
 cttacgcacc tgtcactcaa gtacaacaac ctactgcgg tgccccgcgg cctgcccccc 660
 agcctggagt acctgctatt gtctacaac cacatcatca ccctggcacc tgaggacctg 720
 gccaacctga ccgcctcgc tgtgtcgtat gtgggtggga actgccgtcg ctgtgaccac 780
 gcccgcaacc cctgtatgga gtgcccgaag ggcttccgc acctgcaccc tgacaccttc 840
 agccacctga accacctga aggcctgggt ttgaaggaca gctctctcta caacctgaac 900

```

cccagatggt tccatgccct gggcaacctc atggtgctgg acctgagtga gaacttccta 960
tatgactgca tcacaaaaac cacagccttc cagggcctgg cccagctgcg cagactcaac 1020
ttgtctttca attaccacaa gaagggtgcc ttgtcccacc tgcattctggc gccctccttc 1080
gggagcctgc tctccctgca gcagctggac atgcatggca tcttcttcog ctcgctcagc 1140
gagaccacgc tccggctcgt ggtccacctg cccatgctcc agagtctgca cctgcagatg 1200
aacttcatac atcaggccca gctcagcacc ttccggggcct tccttggcct gcgatacgtg 1260
gacctgtcag acaaccgcat aagtggagcc atggagctgg cggctgccac gggggaggtg 1320
gatggtgggg agagagtccg gctgccatct ggggacctag ctctggggcc accgggcacc 1380
cctagctccg agggcttcat gccaggctgc aagacctca acttcacctt ggacctgtca 1440
cggaacaacc tagtgacaat ccagccagag atgtttgccc ggctctcgcg cctccagtg 1500
ctgtctcctga gccgcaacag catctcgagc gcagtcaacg gctcacaatt tatgccgctg 1560
accagcctgc aggtgctgga cctgtcccat aacaagctgg acctgtacca tgggcgctct 1620
ttcacggagc tgccgcggct ggaggccctg gacctcagct acaacagcca gcccttcagc 1680
atgcagggcg tgggtcacia cctcagcttt gtggcacagc tgccggccct gcgctatctc 1740
agcctggcgc acaacgacat ccacagccgt gtgtcccagc agctctgcag cgcctcgctg 1800
cgggccttgg acttcagcgg caatgccttg agccggatgt gggccgaggg agacctgtat 1860
ctccacttct tccgaggcct gaggagcctg gtccggtttg atctgtccca gaatcgcttg 1920
cataccctct tgccacgcac cctggacaac ctccccaaga gcctgcggct gctgcgtctc 1980
cgtgacaatt atctggcttt cttcaactgg agcagcctgg tcctcctccc caggctggaa 2040
gccctggacc tggcgggaaa ccagctgaag gccctgagca acggcagctt gcctaattgga 2100
accagctcc agaggctgga cctcagcagc aacagtatca gcttcgtggc ctccagcttt 2160
tttgctctgg ccaccaggct gcgagagctc aacctcagtg ccaacgccct caagacgggtg 2220
gagccctcct ggttcgggtc tctagcgggc accctgaaag tcctagatgt gactggcaac 2280
ccctgcact gcgcctgtgg ggcggccttc gtggacttct tgctggaggt gcaggctgca 2340
gtgcccgccc tgccaggcca cgtcaagtgt ggcagtccag gtcagctcca gggccgcagc 2400
atctttgcgc aggatctgag cctctgcctg gatgaggccc tctcctggga ctgttttggc 2460

```

<210> 29

<211> 1032

<212> PRT

<213> Mus musculus

<400> 29

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn
 50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn
 65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met
 100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
 130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
 145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro
 180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu

225		230		235		240
Ala Asn Leu Thr	Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg					
	245			250		255
Arg Cys Asp His	Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser					
	260		265			270
Leu His Leu His	Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly					
	275		280			285
Leu Val Leu Lys	Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe					
	290		295		300	
Gln Gly Leu Val	Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu					
305		310		315		320
Tyr Glu Ser Ile	Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu					
	325			330		335
Arg Lys Leu Asn	Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala					
	340		345			350
Arg Leu His Leu	Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu					
	355		360			365
Leu Asn Met Asn	Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu					
	370		375		380	
Arg Trp Leu Ala	Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met					
385		390		395		400
Asn Phe Ile Asn	Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala					
	405		410			415
Leu Arg Phe Val	Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr					
	420		425			430
Leu Ser Glu Ala	Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu					
	435		440			445
Leu Leu Ser Ala	Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser					
	450		455		460	

Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu
 465 470 475 480

Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
 485 490 495

Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala
 500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp
 515 520 525

Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu
 530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
 545 550 555 560

Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser
 565 570 575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val
 580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly
 595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe
 610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn
 625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu
 645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr
 660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn
 675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
 690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala
 705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn
 725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
 740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly
 755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly
 770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg
 785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser
 805 810 815

Trp Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Met Val
 820 825 830

Val Pro Ile Leu His His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe
 835 840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Ala Arg Ser Arg Arg Ser
 850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln
 865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu
 885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp
 900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr
 915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser
 930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
 980 985 990

Leu Phe Trp Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln
 995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu
 1025 1030

<210> 30
 <211> 821
 <212> PRT
 <213> Mus musculus

<400> 30

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn
 50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn
 65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met
 100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
 130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
 145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro
 180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser
 260 265 270

Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe
 290 295 300

Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu
 325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala

340	345	350
Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu		
355	360	365
Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu		
370	375	380
Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met		
385	390	395
Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala		
405	410	415
Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr		
420	425	430
Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu		
435	440	445
Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser		
450	455	460
Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu		
465	470	475
Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu		
485	490	495
Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala		
500	505	510
Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp		
515	520	525
Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu		
530	535	540
Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe		
545	550	555
Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser		
565	570	575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val
 580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly
 595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe
 610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn
 625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu
 645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr
 660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn
 675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
 690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala
 705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn
 725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
 740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly
 755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly
 770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg
 785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser
 805 810 815

Trp Asp Cys Phe Gly
820

<210> 31
<211> 3200
<212> DNA
<213> Mus musculus

<400> 31
tgtcagaggg agcctcgga gaatcctcca tctcccaaca tggttctccg tcgaaggact 60
ctgcaccctt tgtccctcct ggtacaggct gcagtgtctgg ctgagactct ggccttgggt 120
accctgcctg ccttctacc ctgtgagctg aagcctcatg gcttgggtga ctgcaattgg 180
ctgttctctga agtctgtacc cgtttctctt gcggcagcat cctgtctcaa catcaccgcg 240
cttctccttga tctccaaccg tatccaccac ctgcacaact ccgacttcgt ccacctgtcc 300
aacctgcggc agctgaacct caagtggaa tgtccacca ctggccttag cccctgcac 360
ttctcttgcc acatgaccat tgagcccaga accttcttgg ctatgcgtac actggaggag 420
ctgaacctga gctataatgg tatcaccact gtgccccgac tgcccagctc cctgggtgaat 480
ctgagcctga gccacaccaa catcctggtt ctagatgcta acagcctcgc cggcctatac 540
agcctgcgcg ttctcttcat ggacgggaac tgctactaca agaaccctg cacaggagcg 600
gtgaaggtga cccagggcg cctcctgggc ctgagcaatc tcaccatct gtctctgaag 660
tataacaacc tcacaaaggt gccccgcaa ctgccccca gctggagta cctcctggtg 720
tcctataacc tcattgtcaa gctggggcct gaagacctgg ccaatctgac ctcccttoga 780
gtacttgatg tgggtgggaa ttgccgtcgc tgcgaccatg ccccaatcc ctgtatagaa 840
tgtggccaaa agtccctcca cctgcaccct gagaccttc atcacctgag ccatctggaa 900
ggcctggtgc tgaaggacag ctctctccat aactgaact cttcctggtt ccaaggctctg 960
gtcaacctct cgggtgctga cctaagcgag aactttctct atgaaagcat caaccacacc 1020
aatgcctttc agaacctaac ccgctgcgc aagctcaacc tgccttcaa ttaccgcaag 1080
aaggatcct ttgccgcct ccacctggca agttccttca agaacctgggt gtcaactgcag 1140
gagctgaaca tgaacggcat cttcttccgc tcgctcaaca agtacacgct cagatggctg 1200
gccgatctgc ccaaactcca cactctgcat cttcaaata acttcatcaa ccaggcacag 1260
ctcagcatct ttggtacctt ccgagccctt cgctttgtgg acttgctcaga caatcgcatc 1320
agtgggcctt caacgctgtc agaagccacc cctgaaggag cagatgatgc agagcaggag 1380
gagctgttgt ctgcggatcc tcaccagct ccaactgagca cccctgcttc taagaacttc 1440

atggacaggt gtaagaactt caagttcacc atggacctgt ctcggaacaa cctggtgact	1500
atcaagccag agatgtttgt caatctetca cgcctccagt gtcttagcct gagccacaac	1560
tccattgcac aggetgtcaa tggctctcag ttcttgccgc tgactaatct gcaggtgctg	1620
gacctgtccc ataacaaact ggacttgtac cactggaaat cgttcagtga gctaccacag	1680
ttgcaggccc tggacctgag ctacaacagc cagcccttta gcatgaaggg tataggccac	1740
aatttcagtt ttgtggccca tctgtccatg ctacacagcc ttagcctggc acacaatgac	1800
attcataccc gtgtgtcctc acatctcaac agcaactcag tgaggtttct tgacttcagc	1860
ggcaacggta tgggcccgc atgtgggatgag gggggccttt atctccattt cttccaaggc	1920
ctgagtggcc tgctgaagct ggacctgtct caaaataacc tgcatatcct ccggccccag	1980
aaccttgaca acctcccaa gagcctgaag ctgctgagcc tccgagacaa ctacctatct	2040
ttctttaact ggaccagtct gtcccttctg cccaacctgg aagtcctaga cctggcaggc	2100
aaccagctaa aggcctgac caatggcacc ctgcctaatg gcacctcct ccagaaactg	2160
gatgtcagca gcaacagtat cgtctctgtg gtcccagcct tcttcgctct ggcggtcgag	2220
ctgaaagagg tcaacctcag ccacaacatt ctcaagacgg tggatcgctc ctggtttggg	2280
cccattgtga tgaacctgac agttctagac gtgagaagca accctctgca ctgtgcctgt	2340
ggggcagcct tcgtagactt actgttggag gtgcagacca aggtgcctgg cctggctaata	2400
ggtgtgaagt gtggcagccc cggccagctg cagggccgta gcatcttcgc acaggacctg	2460
cggctgtgcc tggatgaggt cctctcttgg gactgctttg gcctttcact cttggctgtg	2520
gccgtgggca tgggtgtgcc tatactgcac catctctgcg gctgggacgt ctggtactgt	2580
tttcatctgt gcctggcatg gctacctttg ctggcccga gccgacgcag cggccaagct	2640
ctccccatg atgccttcgt ggtgttcgat aaggcacaga gcgcagttgc ggactgggtg	2700
tataacgagc tgcgggtgcg gctggaggag cggcgcggtc gccgagccct acgcttgtgt	2760
ctggaggacc gagattggct gcctggccag acgctcttcg agaacctctg ggcttccatc	2820
tatgggagcc gcaagactct atttgtgctg gccacacgg accgcgtcag tggcctcctg	2880
cgcaccagct tcctgctggc tcagcagcgc ctgttgaag accgcaagga cgtggtggtg	2940
ttggtgatcc tgcgtccgga tgcccacgc tcccgctatg tgcgactgcg ccagcgtctc	3000
tgccgccaga gtgtgctctt ctggccccag cagcccaacg ggcagggggg cttctgggcc	3060
cagctgagta cagccctgac tagggacaac cgccacttct ataaccagaa cttctgccgg	3120
ggacctacag cagaatagct cagagcaaca gctggaaca gctgcatctt catgcctggt	3180
tcccagattg ctctgcctgc	3200

<210> 32
 <211> 2463
 <212> DNA
 <213> Mus musculus

<400> 32
 atggttctcc gtcgaaggac tctgcacccc ttgtccctcc tggtagaggc tgcagtgtg 60
 gctgagactc tggccctggg taccctgcct gccttctac cctgtgagct gaagcctcat 120
 ggccctgggtg actgcaattg gctgttctctg aagtctgtac cccgtttctc tgcggcagca 180
 tctgtctcca acatcacccg cctctccttg atctccaacc gtatccacca cctgcacaac 240
 tccgacttcg tccacctgtc caacctgcgg cagctgaacc tcaagtggaa ctgtccaccc 300
 actggcctta gccccctgca cttctcttgc cacatgacca ttgagcccag aaccttctctg 360
 gctatgcgta cactggagga gctgaacctg agctataatg gtatcaccac tgtgccccga 420
 ctgcccagct ccctgggtgaa tctgagcctg agccacacca acatcctggg tctagatgct 480
 aacagcctcg ccggcctata cagcctgcgc gttctcttca tggacgggaa ctgctactac 540
 aagaacccct gcacaggagc ggtgaagggtg accccaggcg ccctcctggg cctgagcaat 600
 ctcacccatc tgtctctgaa gtataacaac ctcacaaagg tgccccgcca actgcccccc 660
 agcctggagt acctcctggg gtcctataac ctcatgtca agctggggcc tgaagacctg 720
 gccaatctga cctcccttcg agtacttgat gtgggtggga attgccgtcg ctgcgaccat 780
 gcccccaatc cctgtataga atgtggccaa aagtcctctc acctgcaccc tgagaccttc 840
 catcacctga gccatctgga aggcctgggtg ctgaaggaca gctctctcca tacactgaac 900
 tcttctctgg tccaaggtct ggtcaacctc tcgggtgctgg acctaagcga gaactttctc 960
 tatgaaagca tcaaccacac caatgccttt cagaacctaa ccgcctgcg caagctcaac 1020
 ctgtccttca attaccgcaa gaaggatatc tttgcccgc tccacctggc aagttccttc 1080
 aagaacctgg tgtcactgca ggagctgaac atgaacggca tcttcttccg ctgctcaac 1140
 aagtacacgc tcagatggct ggccgatctg cccaaactcc aactctgca tcttcaaattg 1200
 aacttcatca accaggcaca gctcagcatc tttggtacct tccgagccct tcgctttgtg 1260
 gacttgctcag acaatcgcat cagtgggect tcaacgctgt cagaagccac ccctgaagag 1320
 gcagatgatg cagagcagga ggagctgttg tctgcggatc ctacccagc tccactgagc 1380
 acccctgctt ctaagaactt catggacagg tgtaagaact tcaagttcac catggacctg 1440
 tctcggaaca acctggtgac tatcaagcca gagatgtttg tcaatctctc acgcctccag 1500
 tgtcttagcc tgagccacaa ctccattgca caggctgtca atggctctca gttcctgccg 1560


```

ctgactaatc tgcaggtgct ggacctgtcc cataacaaac tggacttgta ccactggaaa 1620
tcgttcagtg agtaccaca gttgcaggcc ctggacctga gctacaacag ccagcccttt 1680
agcatgaagg gtataggcca caatttcagt tttgtggccc atctgtccat gctacacagc 1740
cttagcctgg cacacaatga cattcatacc cgtgtgtcct cacatctcaa cagcaactca 1800
gtgagggtttc ttgacttcag cggcaacggt atgggccgca tgtgggatga ggggggcctt 1860
tatctccatt tcttccaagg cctgagtggc ctgctgaagc tggacctgtc tcaaaataac 1920
ctgcatatcc tccggcccca gaaccttgac aacctcccca agagcctgaa gctgctgagc 1980
ctccgagaca actacctatc tttctttaac tggaccagtc tgtccttctt gcccaacctg 2040
gaagtccctag acctggcagg caaccagcta aaggccctga ccaatggcac cctgcctaata 2100
ggcacccctcc tccagaaact ggatgtcagc agcaacagta tcgtctctgt ggtcccagcc 2160
ttcttcgctc tggcggtcga gctgaaagag gtcaacctca gccacaacat tctcaagacg 2220
gtggatcgct cctggtttgg gccatttgtg atgaacctga cagttctaga cgtgagaagc 2280
aacctctctg actgtgcctg tggggcagcc ttcgtagact tactgttgga ggtgcagacc 2340
aagggtgcctg gcctggctaa tgggtgtgaag tgtggcagcc ccggccagct gcagggccgt 2400
agcatcttcg cacaggacct gcggctgtgc ctggatgagg tcctctcttg ggactgcttt 2460
ggc 2463

```

```

<210> 33
<211> 1032
<212> PRT
<213> Homo sapiens

```

```

<400> 33

```

```

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln
1           5           10           15

```

```

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20           25           30

```

```

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
35           40           45

```

```

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn
50           55           60

```

```

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp
65           70           75           80

```

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met
 100 105 110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
 115 120 125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser
 130 135 140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser
 145 150 155 160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr
 210 215 220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe
 260 265 270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe
 290 295 300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu

305	310	315	320
Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu	325	330	335
Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala	340	345	350
His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu	355	360	365
Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu	370	375	380
Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met	385	390	395
Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly	405	410	415
Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu	420	425	430
Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu	435	440	445
Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu	450	455	460
Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser	465	470	475
Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser	485	490	495
His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val	500	505	510
Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu	515	520	525
Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu	530	535	540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly
 545 550 555 560

Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr
 565 570 575

Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser
 580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
 595 600 605

Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe
 610 615 620

Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu
 625 630 635 640

His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln
 645 650 655

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser
 660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg
 675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg
 690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe
 705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
 725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu
 740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
 755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
805 810 815

Asp Cys Phe Ala Leu Ser Leu Leu Ala Val Ala Leu Gly Leu Gly Val
820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His
835 840 845

Leu Cys Leu Ala Trp Leu Pro Trp Arg Gly Arg Gln Ser Gly Arg Asp
850 855 860

Glu Asp Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Thr Gln
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Gly Gln Leu Glu
885 890 895

Glu Cys Arg Gly Arg Trp Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp
900 905 910

Trp Leu Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser
930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Gly Arg
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln
995 1000 1005

Leu Gly Met Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg
1010 1015 1020

Asn Phe Cys Gln Gly Pro Thr Ala Glu
1025 1030

<210> 34
<211> 820
<212> PRT
<213> Homo sapiens

<400> 34

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn
50 55 60

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp
65 70 75 80

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser
130 135 140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser
145 150 155 160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr
 210 215 220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe
 260 265 270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe
 290 295 300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu
 325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala
 340 345 350

His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu
 370 375 380

Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu

420	425	430
Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu		
435	440	445
Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu		
450	455	460
Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser		
465	470	475
Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser		
485	490	495
His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val		
500	505	510
Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu		
515	520	525
Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu		
530	535	540
Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly		
545	550	555
Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr		
565	570	575
Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser		
580	585	590
Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn		
595	600	605
Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe		
610	615	620
Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu		
625	630	635
His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln		
645	650	655

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser
660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg
675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg
690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe
705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu
740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
805 810 815

Asp Cys Phe Ala
820

<210> 35

<211> 3352

<212> DNA

<213> Homo sapiens

<400> 35

aggctggtat aaaaatctta cttcctctat tctctgagcc gctgctgccc ctgtgggaag 60

ggacctcgag tgtgaagcat ccttcctgt agctgctgtc cagtctgccc gccagaccct 120

ctggagaagc ccctgcccc cagcatgggt ttctgccgca gcgcctgca cccgctgtct 180

ctcctgggtgc aggccatcat gctggccatg accctggccc tgggtacett gcctgccttc 240

ctaccctgtg agctccagcc ccacggcctg gtgaactgca actggctgtt cctgaagtct 300

gtgccccact tctccatggc agcaccccggt ggcaatgtca ccagcctttc cttgtcctcc 360
 aaccgcatcc accacctcca tgattctgac ttgcccacc tgcccagcct gcggcatctc 420
 aacctcaagt ggaactgccc gccggttggtc ctcagcccca tgcacttccc ctgccacatg 480
 accatcgagc ccagcacctt cttggctgtg cccaccctgg aagagctaaa cctgagctac 540
 aacaacatca tgactgtgcc tgcgctgccc aaatccctca tatccctgtc cctcagccat 600
 accaacatcc tgatgctaga ctctgccagc ctgcgcggcc tgcattgccct gcgcttcccta 660
 ttcatggacg gcaactgtta ttacaagaac ccctgcaggc aggcactgga ggtggccccg 720
 ggtgccctcc ttggcctggg caacctcacc cacctgtcac tcaagtacaa caacctcact 780
 gtggtgcccc gcaacctgcc ttccagcctg gagtatctgc tgttgctcta caaccgcatc 840
 gtcaaactgg cgctgagga cctggccaat ctgaccgccc tgcgtgtgct cgatgtgggc 900
 ggaaattgcc gccgctgcga ccacgtctcc aacccctgca tggagtgcct tcgtcacttc 960
 cccagctac atcccgatac cttcagccac ctgagccgtc ttgaaggcct ggtgttgaag 1020
 gacagttctc tctcctgggt gaatgccagt tggttccgtg ggctgggaaa cctccgagtg 1080
 ctggacctga gtgagaactt cctctacaaa tgcattcacta aaaccaaggc cttccagggc 1140
 ctaacacagc tgcgcaagct taacctgtcc ttcaattacc aaaagagggt gtcctttgcc 1200
 cacctgtctc tggccccctc cttcgggagc ctggtcgccc tgaaggagct ggacatgcac 1260
 ggcattctct tccgtcact cgatgagacc acgctccggc cactggcccc cctgcccattg 1320
 ctccagactc tgcgtctgca gatgaacttc atcaaccagg cccagctcgg catcttcagg 1380
 gccttccctg gcctgcgcta cgtggacctg tcggacaacc gcatcagcgg agcttcggag 1440
 ctgacagcca ccatggggga ggcagatgga ggggagaagg tctggctgca gcctggggac 1500
 cttgtctcgg cccagtgga cactcccagc tctgaagact tcaggcccaa ctgcagcacc 1560
 ctcaacttca ccttggatct gtcacggaac aacctggtga ccgtgcagcc ggagatgttt 1620
 gccagctct cgcacctgca gtgcctgctc ctgagccaca actgcatctc gcaggcagtc 1680
 aatggctccc agttcctgcc gctgaccggt ctgcaggtgc tagacctgtc ccgcaataag 1740
 ctggacctct accacgagca ctcatcacg gagctaccgc gactggaggc cctggacctc 1800
 agctacaaca gccagccctt tggcatgcag gccgtgggccc acaacttcag cttcgtggct 1860
 cacctgcgca ccctgcgcca cctcagcctg gccacaaca acatccacag ccaagtgtcc 1920
 cagcagctct gcagtacgtc gctgcgggccc ctggacttca gcggcaatgc actgggcat 1980
 atgtggggccg agggagacct ctatctgcac ttcttccaag gcctgagcgg tttgatctgg 2040

ctggacttgt cccagaaccg cctgcacacc ctctgcccc aaacctgcg caacctcccc 2100
 aagagcctac aggtgctgcg tctccgtgac aattacctgg ccttctttaa gtgggtggagc 2160
 ctccacttcc tgcccaaact ggaagtctc gacctggcag gaaaccggct gaaggccctg 2220
 accaatggca gcctgcctgc tggcaccggg ctccggaggc tggatgtcag ctgcaacagc 2280
 atcagcttcg tggcccccgg cttcttttcc aaggccaagg agctgcgaga gctcaacctt 2340
 agcgccaacg ccctcaagac agtggaccac tcctggtttg gggccctggc gagtgccttg 2400
 caaatactag atgtaagcgc caacctctg cactgcgcct gtggggcggc ctttatggac 2460
 ttcttctggtg aggtgcaggc tgccgtgccc ggtctgccc gccgggtgaa gtgtggcagt 2520
 ccggggccagc tccagggcct cagcatcttt gcacaggacc tgcgcctctg cctggatgag 2580
 gccctctcct gggactgttt cgccctctcg ctgctggctg tggctctggg cctgggtgtg 2640
 cccatgctgc atcacctctg tggctgggac ctctggtact gcttccacct gtgcctggcc 2700
 tggcttccct ggcgggggcg gcaaagtggg cgagatgagg atgccctgcc ctacgatgcc 2760
 ttctgtgtct tgcacaaac gcagagcgca gtggcagact ggggtgtacaa cgagcttcgg 2820
 gggcagctgg aggagtgccg tgggcgctgg gactccgcc tgtgcctgga ggaacgcgac 2880
 tggctgcctg gcaaaaccct ctttgagaac ctgtgggcct cggtctatgg cagccgcaag 2940
 acgctgtttg tgctggccca cacggaccgg gtcagtggtc tcttgcgcg cagcttcctg 3000
 ctggcccagc agcgctctgt ggaggaccgc aaggacgtcg tgggtgctggt gatcctgagc 3060
 cctgacggcc gccgctccc ctacgtgcgg ctgcgccagc gcctctgccg ccagagtgtc 3120
 ctctctggc cccaccagcc cagtggtcag cgcagcttct gggcccagct gggcatggcc 3180
 ctgaccaggg acaaccacca cttctataac cggaacttct gccagggacc cacggccgaa 3240
 tagcgtgag ccggaatcct gcacggtgcc acctccacac tcacctacc tctgcctgcc 3300
 tggctgacc ctccctgct cgctccctc accccacacc tgacacagag ca 3352

<210> 36

<211> 2460

<212> DNA

<213> Homo sapiens

<400> 36

atgggtttct gccgcagcgc cctgcacccg ctgtctctcc tgggtgcaggc catcatgctg 60
 gccatgacct tggccctggg taccttgctt gccttcctac cctgtgagct ccagccccac 120
 ggcctggtga actgcaactg gctgttcttg aagtctgtgc cccacttctc catggcagca 180
 ccccgtagga atgtcaaccg cctttccttg tcctccaacc gcatccacca cctccatgat 240

tctgactttg cccacctgcc cagcctgcgg catctcaacc tcaagtggaa ctgcccgcg 300
 gttggcctca gcccctatgca cttcccctgc cacatgacca tcgagcccag caccttcttg 360
 gctgtgcca ccctggaaga gctaaacctg agctacaaca acatcatgac tgtgcctgcg 420
 ctgccc aaat ccctcatatc cctgtccctc agccatacca acatcctgat gctagactct 480
 gccagcctcg ccggcctgca tgcctgcgc ttcctattca tggacggcaa ctgttattac 540
 aagaaccct gcaggcaggc actggagggtg gcccgggtg ccctccttg cctgggcaac 600
 ctcaccacc tgctactcaa gtacaacaac ctactgttg tgcgcgcaa cctgccttcc 660
 agcctggagt atctgctgtt gtctacaac cgcactgtca aactggcgcc tgaggacctg 720
 gccaatctga ccgcctgcg tgtgctgat gtggcgga attgccgcg ctgcgaccac 780
 gctcccaacc cctgcatgga gtgcctcgt cacttcccc agctacatcc cgataccttc 840
 agccacctga gccgtcttga aggcctgggtg ttgaaggaca gttctctctc ctggctgaat 900
 gccagtgggt tccgtgggt gggaaacctc cgagtgttg acctgagtga gaacttctc 960
 taaaaatgca tcaactaaaac caaggccttc cagggcctaa cacagctgcg caagcttaac 1020
 ctgtccttca attacaaaa gaggtgtcc tttgccacc tgtctctggc cccttcttc 1080
 gggagccttg tcgccctgaa ggagctggac atgcacggca tcttcttccg ctactcgat 1140
 gagaccacgc tccggccact ggccgcctg cccatgtcc agactctgcg tctgcagatg 1200
 aacttcatca accaggccca gctcggcatc ttcagggcct tccctggcct gcgctacgtg 1260
 gacctgtcgg acaaccgcat cagcggagct tcggagctga cagccaccat gggggaggca 1320
 gatggagggg agaaggtctg gctgcagcct ggggaccttg ctccggcccc agtggacact 1380
 cccagctctg aagacttcag gcccactgc agcaccctca acttcacctt ggatctgtca 1440
 cggacaacc tggtgaccgt gcagcggag atgtttgcc agctctcgca cctgcagtgc 1500
 ctgcgcctga gccacaactg catctcgag gcagtcaatg gctcccagtt cctgccgctg 1560
 accggtctgc aggtgctaga cctgtccgc aataagctgg acctctacca cgagcactca 1620
 ttcacggagc taccgcgact ggaggcctg gacctcagct acaacagcca gcccttggc 1680
 atgcaggcg tgggccacaa cttcagcttc gtggctcacc tgcgcaccct gcgccacctc 1740
 agcctggccc acaacaacat ccacagccaa gtgtcccagc agctctgcag tacgtcgctg 1800
 cgggccttg acttcagcg caatgcactg ggccatatgt gggccgagg agacctctat 1860
 ctgcacttct tccaaggcct gagcggttg atctggctgg acttgtcca gaaccgctg 1920
 cacaccctcc tgcccaaac cctgcgcaac ctcccaaga gcctacagg gctgcgtctc 1980
 cgtgacaatt acctggcctt cttaagtgg tggagcctcc acttctgcc caaactggaa 2040

gtcctcgacc tggcaggaaa ccggctgaag gccctgacca atggcagcct gcctgctggc 2100
 acccggtctc ggaggtgga tgtcagctgc aacagcatca gcttcgtggc ccccggttc 2160
 tttccaagg ccaaggagct gcgagagctc aaccttagcg ccaacgccct caagacagtg 2220
 gaccactcct ggtttgggccc cctggcgagt gccctgcaaa tactagatgt aagcgccaac 2280
 cctctgcaact gcgcctgtgg ggcggccttt atggacttcc tgetggaggt gcaggctgcc 2340
 gtgcccggtc tgcccagccg ggtgaagtgt ggcagtcgg gccagctcca gggcctcagc 2400
 atctttgcac aggacctgcg cctctgcctg gatgaggccc tctcctggga ctgtttcgcc 2460

<210> 37
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 37
 accttgctg ccttcctacc ctgtga 26

<210> 38
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 38
 gtccgtgtgg gccagcaca a 21

<210> 39
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 39
 tccatgacgt ttttgatgtt 20

<210> 40
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 40
tccataacgt ttttgatggt 20

<210> 41
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 41
tccatcacgt ttttgatggt 20

<210> 42
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 42
tccattacgt ttttgatggt 20

<210> 43
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 43
tccatggcgt ttttgatggt 20

<210> 44
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 44
tccatgccgt ttttgatggt 20

<210> 45
<211> 20
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 45

tccatgtcgt ttttgatggt

20

<210> 46

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 46

tccatgatgt ttttgatggt

20

<210> 47

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 47

tccatgaagt ttttgatggt

20

<210> 48

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 48

tccatgaggt ttttgatggt

20

<210> 49

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 49

tccatgacat ttttgatggt

20

<210> 50

<211> 20

<212> DNA

<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 50
tccatgacct ttttgatggt 20

<210> 51
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 51
tccatgactt ttttgatggt 20

<210> 52
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 52
tccatgacgc ttttgatggt 20

<210> 53
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 53
tccatgacga ttttgatggt 20

<210> 54
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 54
tccatgacgg ttttgatggt 20

<210> 55
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 55
tccatgacgt ctttgatggt 20

<210> 56
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 56
tccatgacgt atttgatggt 20

<210> 57
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 57
tccatgacgt gtttgatggt 20

<210> 58
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 58
tcgtcgtttt gtcgttttgt cggt 24

<210> 59
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 59
tgctgctttt gtgcttttgt gctt 24

<210> 60
<211> 20
<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 60

tccatgacgt tcctgatgct

20

<210> 61

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 61

tccatgagct tcctgatgct

20

<210> 62

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> Consensus oligopeptide

<220>

<221> MISC_FEATURE

<222> (4)..(5)

<223> Any amino acid

<220>

<221> MISC_FEATURE

<222> (7)..(12)

<223> Any amino acid

<220>

<221> MISC_FEATURE

<222> (14)..(15)

<223> Any amino acid

<400> 62

Gly Asn Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
1 5 10 15

<210> 63

<211> 16

<212> PRT

<213> Homo sapiens

<400> 63

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys
 1 5 10 15

<210> 64
 <211> 16
 <212> PRT
 <213> Mus musculus

<400> 64

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Ile Cys
 1 5 10 15

<210> 65
 <211> 31
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Consensus oligopeptide

<220>
 <221> MISC_FEATURE
 <222> (2)..(8)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (10)..(10)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (12)..(12)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (14)..(22)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (25)..(30)
 <223> Any amino acid

<400> 65

Arg Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Asp Xaa Tyr Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Ser Xaa Xaa Xaa Xaa Xaa Xaa Tyr
 20 25 30

<210> 66
 <211> 31
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (2)..(8)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (10)..(10)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (12)..(12)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (14)..(22)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (25)..(30)
 <223> Any amino acid

<400> 66

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Tyr
 20 25 30

<210> 67
 <211> 31
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (2)..(8)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (10)..(10)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (12)..(12)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (14)..(22)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (25)..(30)
 <223> Any amino acid

<400> 67

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Gln Leu Xaa Xaa Xaa Xaa Xaa Tyr
 20 25 30

<210> 68
 <211> 31
 <212> PRT
 <213> Homo sapiens

<400> 68

Gln Val Leu Asp Leu Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His
 1 5 10 15

Ser Phe Thr Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr
 20 25 30

<210> 69
 <211> 31
 <212> PRT
 <213> Mus musculus

<400> 69

Gln Val Leu Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys

```
<210> 70
<211> 20
<212> DNA
<213> Artificial sequence
```

<400> 70
tccaggactt ctctcagggtt